

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 27, 2005, 11:51:56 ; Search time 165 seconds
(without alignments)
525.057 Million cell updates/sec

Title: US-10-623-429-9_COPY_404_627

Perfect score: 1237

Sequence: 1 AIAADROAGGLPAAAGDHGI.....ALVNASSAAHVNVDTARAAD 224

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|------------|--------------------|
| 1 | 1237 | 100.0 | 329 | 6 AAE36429 | Aae36429 HSV-2 UL2 |
| 2 | 1237 | 100.0 | 637 | 6 AAE36428 | Aae36428 HSV-2 UL2 |
| 3 | 1237 | 100.0 | 637 | 8 ADJ77800 | Adj77800 Herpes si |
| 4 | 1233 | 99.7 | 331 | 2 AAR64769 | Aar64769 HSV-2 ISP |
| 5 | 1233 | 99.7 | 636 | 2 AAR64767 | Aar64767 HSV-2 pro |
| 6 | 1233 | 99.7 | 638 | 2 AAR71017 | Aar71017 HSV-2 pro |
| 7 | 1233 | 99.7 | 642 | 2 AAW72124 | Aaw72124 HSV-2 str |
| 8 | 1228 | 99.3 | 252 | 2 AAW72049 | Aaw72049 HSV-2 str |
| 9 | 1189 | 96.1 | 657 | 2 AAR72192 | Aar72192 HSV-2 str |
| 10 | 670.5 | 54.2 | 635 | 7 AAR71031 | Aar71031 HSV-1 UL2 |
| 11 | 670.5 | 54.2 | 635 | 7 ADL18166 | Adl18166 Human her |
| 12 | 666.5 | 53.9 | 415 | 2 AAR28638 | Aar28638 UL26 prot |
| 13 | 666.5 | 53.9 | 603 | 2 AAR28641 | Aar28641 UL26 prot |
| 14 | 666.5 | 53.9 | 626 | 2 AAR28640 | Aar28640 UL26 prot |
| 15 | 666.5 | 53.9 | 635 | 2 AAR28634 | Aar28634 UL26 prot |
| 16 | 666.5 | 53.9 | 635 | 2 AAR28649 | Aar28649 UL26 prot |
| 17 | 666.5 | 53.9 | 635 | 2 AAR28647 | Aar28647 UL26 prot |
| 18 | 666.5 | 53.9 | 635 | 2 AAR28651 | Aar28651 UL26 prot |
| 19 | 666.5 | 53.9 | 635 | 2 AAR28648 | Aar28648 UL26 prot |
| 20 | 666.5 | 53.9 | 635 | 2 AAR28650 | Aar28650 UL26 prot |
| 21 | 666.5 | 53.9 | 635 | 2 AAR28652 | Aar28652 UL26 prot |
| 22 | 666.5 | 53.9 | 636 | 2 AAR28635 | Aar28635 UL26 prot |
| 23 | 661 | 53.4 | 636 | 2 AAR28636 | Aar28636 UL26 prot |
| 24 | 656 | 53.0 | 636 | 2 AAR28637 | Aar28637 UL26 prot |
| 25 | 623.5 | 50.4 | 615 | 2 AAR28642 | Aar28642 UL26 prot |

ALIGNMENTS

RESULT 1

AAE36429
ID AAE36429 standard; protein; 329 AA.

AC AAE36429;

XX 07-AUG-2003 (first entry)

XX HSV-2 UL26.5 full-length antigen.

XX Herpes simplex virus; HSV; infection; vaccine; therapy; UL26.5; antigen.

XX Herpes simplex virus type 2.

XX WO2003020108-A2.

XX 13-MAR-2003.

XX 27-AUG-2002; 2002WO-US027341.

XX 04-SEP-2001; 2001US-0317159P.

XX 17-APR-2002; 2002US-0373429P.

XX (CORI-) CORIXA CORP.

XX Hosken NA, Day CH;

XX WPI, 2003-290135/28.

XX N-PSDB; AAD55178.

Novel isolated polypeptide comprising immunogenic portion of a herpes simplex virus antigen, useful for detecting herpes simplex virus infection in a subject, and for treating the virus infection in a patient.

Claim 1; Page 112; 114pp; English.

The invention relates to polypeptides comprising an immunogenic portion of herpes simplex virus (HSV) antigen and to nucleic acid molecules encoding polypeptides. Polypeptides of the invention are useful for detecting and treating HSV infection in a patient. Polynucleotides of the invention are useful as diagnostic reagents for detecting HSV infection in a patient and also as a probes or primers. The invention is used to prepare vaccines. The present sequence is HSV-2 strain HG52 UL26.5 full-length antigen

Sequence 329 AA;

Db 404 ATAADROAGGLPAAAGDHGIRGSAKRREHEVEQPEYDCGRDEPRDRFPFYFGEARPEPRP 463
QY 61 VDSRAARQASGPHETITLVCVAVTSLOQELAHMRARTHAPYGPYPVPGYHHPHADTET 120
Db 464 VDSRAARQASGPHETITLVCVAVTSLOQELAHMRARTHAPYGPYPVPGYHHPHADTET 523
QY 121 PAQPPRYPAKAVYLPPLPHIAPPGLPSGAVPPSPYPVAVTGPAPPLHQPSPAHAPPP 180
Db 524 PAQPPRYPAKAVYLPPLPHIAPPGLPSGAVPPSPYPVAVTGPAPPLHQPSPAHAPPP 583
QY 181 PPPGTPPPAASLPQEPAPGAEGALVNASSAAHVNVDTARAAD 224
Db 584 PPPGTPPPAASLPQEPAPGAEGALVNASSAAHVNVDTARAAD 627

RESULT 4

AAR64769
ID AAR64769 standard; protein; 331 AA.

XX AC AAR64769;

XX XX 25-MAR-2003 (revised)
DT 19-JUL-1995 (first entry)

XX DE HSV-2 ISP35 protein.

XX KW Protease; HSV-2; protease-inhibitor; virucide; ISP35.

XX OS Herpes simplex virus type 2.

XX PN WO9429456-A2.

XX XX 22-DEC-1994.

XX PF 25-MAY-1994; 94WO-US005920.

XX PR 08-JUN-1993; 93US-00073819.

XX PR 23-MAY-1994; 94US-00245390.

XX XX (ABBO) ABBOTT LAB.

XX PI Steffy KR, Kati WM, Katz L, Mcgonigal TP, Sarthy AV, Schoen SE;

XX DR WPI; 1995-036483/05.

XX DR N-PSDB; AAQ76261.

XX PT New Herpes Simplex Virus type 2 protease - used in screening methods for identifying potential herpes viral protease inhibitor cpds.

XX PS Disclosure; Page 32-34; 56pp; English.

XX CC HSV-2 DNA (given in'AAQ76252) was isolated from Vero cells infected with HSV-2 strain Ci. The translated amino acid sequence is given in AAR64767. The DNA was digested with BamHI, sepd. by gel electrophoresis and transferred to nitrocellulose. A nick-translated probe deriv. from HSV-1 protease was used for hybridization to identify DNA (AAQ76261) encoding HSV-2 protease (AAR64768) and the protease substrate ICP35 (AAR64769). (Updated on 25-MAR-2003 to correct PN field.)

XX XX Sequence 331 AA;

Query Match 99.7%; Score 1233; DB 2; Length 331;
Best Local Similarity 99.6%; Pred. No. 2.7e-84;
Matches 223; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAADROAGGLPAAAGDHGIRGSAKRREHEVEQPEYDCGRDEPRDRFPFYFGEARPEPRP 60
Db 98 ATAADROAGGLPAAAGDHGIRGSAKRREHEVEQPEYDCGRDEPRDRFPFYFGEARPEPRP 157

QY 61 VDSRAARQASGPHETITLVCVAVTSLOQELAHMRARTHAPYGPYPVPGYHHPHADTET 120
Db 158 VDSRAARQASGPHETITLVCVAVTSLOQELAHMRARTHAPYGPYPVPGYHHPHADTET 217

QY 121 PAQPPRYPAKAVYLPPLPHIAPPGLPSGAVPPSPYPVAVTGPAPPLHQPSPAHAPPP 180
Db 218 PAQPPRYPAEAVYLPPLPHIAPPGLPSGAVPPSPYPVAVTGPAPPLHQPSPAHAPPP 277
QY 181 PPPGTPPPAASLPQEPAPGAEGALVNASSAAHVNVDTARAAD 224
Db 278 PPPGTPPPAASLPQEPAPGAEGALVNASSAAHVNVDTARAAD 321

RESULT 5

AAR64767

ID AAR64767 standard; protein; 636 AA.

XX AC AAR64767;

XX XX 25-MAR-2003 (revised)
DT 19-JUL-1995 (first entry)

XX XX HSV-2 protease, ICP35.

XX KW Protease; HSV-2; protease-inhibitor; virucide; ICP35.

XX OS Herpes simplex virus type 2.

XX PN WO9429456-A2.

XX PD 22-DEC-1994.

XX PF 25-MAY-1994; 94WO-US005920.

XX PR 08-JUN-1993; 93US-00073819.

XX PR 23-MAY-1994; 94US-00245390.

XX XX (ABBO) ABBOTT LAB.

XX PI Steffy KR, Kati WM, Katz L, Mcgonigal TP, Sarthy AV, Schoen SE;

XX DR WPI; 1995-036483/05.

XX DR N-PSDB; AAQ76252.

XX PT New Herpes Simplex Virus type 2 protease - used in screening methods for identifying potential herpes viral protease inhibitor cpds.

XX PS Claim 4; Fig 1A-1C; 56pp; English.

XX CC HSV-2 DNA (given in AAQ76252) was isolated from Vero cells infected with HSV-2 strain Ci. The translated amino acid sequence is given in AAR64767. The DNA was digested with BamHI, sepd. by gel electrophoresis and transferred to nitrocellulose. A nick-translated probe deriv. from HSV-1 protease was used for hybridization to identify DNA (AAQ76261) encoding HSV-2 protease (AAR64768) and the protease substrate ICP35 (AAR64769). (Updated on 25-MAR-2003 to correct PN field.)

XX XX Sequence 636 AA;

Query Match 99.7%; Score 1233; DB 2; Length 636;
Best Local Similarity 99.6%; Pred. No. 5.1e-84;
Matches 223; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATAADROAGGLPAAAGDHGIRGSAKRREHEVEQPEYDCGRDEPRDRFPFYFGEARPEPRP 60
Db 403 ATAADROAGGLPAAAGDHGIRGSAKRREHEVEQPEYDCGRDEPRDRFPFYFGEARPEPRP 462

QY 61 VDSRAARQASGPHETITLVCVAVTSLOQELAHMRARTHAPYGPYPVPGYHHPHADTET 120
Db 463 VDSRAARQASGPHETITLVCVAVTSLOQELAHMRARTHAPYGPYPVPGYHHPHADTET 522

QY 121 PAQPPRYPAKAVYLPPLPHIAPPGLPSGAVPPSPYPVAVTGPAPPLHQPSPAHAPPP 180
Db 523 PAQPPRYPAEAVYLPPLPHIAPPGLPSGAVPPSPYPVAVTGPAPPLHQPSPAHAPPP 582

QY 181 PPPGTPPPAASLPQEPAPGAEGALVNASSAAHVNVDTARAAD 224
Db 181 PPPGTPPPAASLPQEPAPGAEGALVNASSAAHVNVDTARAAD 321

Db 583 PPGGTPPPAASLPQEPAPGAEGALVNASSAAHVNDTARAAD 626

RESULT 6

AA71017
ID AAR71017 standard; protein; 638 AA.

XX AC AAR71017;

XX DT 25-MAR-2003 (revised)

XX DT 02-OCT-1995 (first entry)

XX XX HSV-2 protease.

XX XX

XX KW Herpes simplex virus; HSV-2; capsid; UL26 gene.

XX OS Herpes simplex virus type 2.

XX XX WO9506055-A1.

XX XX 02-MAR-1995.

XX PF 19-AUG-1994; 94WO-US009303.

XX PR 20-AUG-1993; 93US-00110522.

XX PR 23-JUN-1994; 94US-00264537.

XX XX (SMIK) SMITHKLINE BEECHAM CORP.

XX PI Dillella AG, Debouck CW;

XX DR WPI; 1995-106803/14.

XX DR N-PSDB; AAQ84671.

XX PT New herpes simplex virus (HSV)-2 protease and capsid protein - used to develop prods. for use in the diagnosis and treatment of HSV-2 infections.

XX PS Claim 1; Fig 1; 51pp; English.

XX XX The sequence is the product of the herpes simplex virus type 2 gene UL26, which is the HSV-2 protease. The protein can be used in the diagnosis and treatment of HSV-2 infections. See also AAR71018-31. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 638 AA;

Query Match 99.7%; Score 1233; DB 2; Length 638;
Best Local Similarity 99.6%; Pred. No. 5.2e-84;
Matches 223; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AIAADROAGGLPAAAGDHGIRGSAKRREHEVEQPEYDCGRDEPDPRDPFYYPGEARPEPRP 60

Db 405 AIAADROAGGLPAAAGDHGIRGSAKRREHEVEQPEYDCGRDEPDPRDPFYYPGEARPEPRP 464

Qy 61 VDSRRARQASGPHETITLVGAVTSLQQLAHMRARTHAPYGPYPVGYHHPHADTET 120

Db 465 VDSRRARQASGPHETITLVGAVTSLQQLAHMRARTHAPYGPYPVGYHHPHADTET 524

Qy 121 PAQPRYPKAVYLPPIPHIAPPGLSGAVPPSPYPVAVTPGAPPLHQPSPAHAHPPP 180

Db 525 PAQPRYPKAVYLPPIPHIAPPGLSGAVPPSPYPVAVTPGAPPLHQPSPAHAHPPP 584

Qy 181 PPGGTPPPAASLPQEPAPGAEGALVNASSAAHVNDTARAAD 224

Db 585 PPGGTPPPAASLPQEPAPGAEGALVNASSAAHVNDTARAAD 628

RESULT 7

AA72124

ID AAW72124 standard; protein; 642 AA.

XX AC AAW72124;

XX DT 18-DEC-1998 (first entry)

XX DE HSV-2 strain SB5 Contig ID 15 ORF#11 protein.

XX KW HSV-2 strain SB5; immunological response induction; therapy: antiviral identification; viral protein inhibitor.

XX KW Herpes simplex virus 2.

XX OS

XX XX WO9820016-A1.

XX XX 14-MAY-1998.

XX XX 31-OCT-1997; 97WO-US020016.

XX PR 04-NOV-1996; 96US-0030279P.

XX PR 09-JUN-1997; 97US-0049018P.

XX XX (SMIK) SMITHKLINE BEECHAM CORP.

XX XX Esser XM, Chan JY, Dabrowski-Amaral CE, Delvecchio AM, Dillon SB;

XX PI Leary JJ;

XX XX WPI; 1998-286847/25.

XX DR N-PSDB; AAV62159.

XX XX Herpes simplex virus type-2 sequences - useful in, e.g. prevention and treatment of infection or inducing immunological response in mammal.

XX PS Claim 10; Page 92; 748pp; English.

XX CC This sequence represents a Herpes simplex virus type-2 (HSV-2) protein

CC SB5 (deposited as ATCC VR-2546) DNA fragment designated Contig ID 15.

CC Based on homology, this sequence is a UL26 protein. The proteins can be

CC used for the treatment or prevention of disease, to induce an

CC immunological response in a mammal or to identify inhibitors, activators

CC or novel antivirals. Antagonists of the proteins can be used to inhibit a

CC viral polypeptide. The DNA sequence or a vector containing it can also be

CC used to induce an immunological response in a mammal

XX SQ Sequence 642 AA;

Query Match 99.7%; Score 1233; DB 2; Length 642;

Best Local Similarity 99.6%; Pred. No. 5.2e-84;

Matches 223; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AIAADROAGGLPAAAGDHGIRGSAKRREHEVEQPEYDCGRDEPDPRDPFYYPGEARPEPRP 60

Db 409 AIAADROAGGLPAAAGDHGIRGSAKRREHEVEQPEYDCGRDEPDPRDPFYYPGEARPEPRP 468

Qy 61 VDSRRARQASGPHETITLVGAVTSLQQLAHMRARTHAPYGPYPVGYHHPHADTET 120

Db 469 VDSRRARQASGPHETITLVGAVTSLQQLAHMRARTHAPYGPYPVGYHHPHADTET 528

Qy 121 PAQPRYPKAVYLPPIPHIAPPGLSGAVPPSPYPVAVTPGAPPLHQPSPAHAHPPP 180

Db 529 PAQPRYPKAVYLPPIPHIAPPGLSGAVPPSPYPVAVTPGAPPLHQPSPAHAHPPP 588

Qy 181 PPGGTPPPAASLPQEPAPGAEGALVNASSAAHVNDTARAAD 224

Db 589 PPGGTPPPAASLPQEPAPGAEGALVNASSAAHVNDTARAAD 632

RESULT 8

AA72049

ID AAW72049 standard; protein; 252 AA.

XX AC AAW72049;

XX XX

XX DT 07-DEC-1998 (first entry)

XX XX

Fri Jul 29 10:53:41 2005

DE HSV-2 strain SB5 Contig ID 104 ORF#17 protein.
XX HSV-2 strain SB5; immunological response induction; therapy;
KW antiviral identification; viral protein inhibitor.
XX
XX OS Herpes simplex virus 2.
XX WO9820016-A1.
XX
XX PD 14-MAY-1998.
XX
XX PF 31-OCT-1997; 97WO-US020016.
XX
XX PR 04-NOV-1996; 96US-0030279P.
XX
XX PR 09-JUN-1997; 97US-0049018P.
XX
XX PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
XX ESser KM, Chan JY, Dabrowski-Amaral CE, Delvecchio AM, Dillon SB;
PI Leary JJ;
XX
XX WPI: 1998-286847/25.
XX
XX DR N-PSDB; AAV62134.
XX
XX PT Herpes simplex virus type-2 sequences - useful in, e.g. prevention and
PT treatment of infection or inducing immunological response in mammal.
XX
XX PS Claim 10; Page 58-59; 748pp; English.
XX
XX CC This sequence represents a Herpes simplex virus type-2 (HSV-2) protein
CC sequence of the invention. This sequence was isolated from a HSV-2 strain
CC SB5 (deposited as ATCC VR-2546) DNA fragment designated Contig ID 104.
CC Based on homology, this sequence is a UL26 protease. The proteins can be
CC used for the treatment or prevention of disease, to induce an
CC immunological response in a mammal or to identify inhibitors, activators
CC or novel antivirals. Antagonists of the proteins can be used to inhibit a
CC viral polypeptide. The DNA sequence or a vector containing it can also be
CC used to induce an immunological response in a mammal
XX
XX SQ Sequence 252 AA;
Query Match 99.3%; Score 1228; DB 2; Length 252;
Best Local Similarity 99.1%; Pred. No. 5e-84;
Matches 222; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 AIAADROAGGLPAAAGDHGIRGSAKRRRHEVEQPEYDCGRDEPDRDFPYPGEARPEPRP 60
DB 19 AIAADROAGGLPAAAGDHGIRGSAKRRRHEVEQPEYDCGRDEPDRDFPYPGEARPEPRP 78
QY 61 VDSRRAARQASGPHETITATVGAVTSLQQLAHMRARTHAPYGPYPVPVGYHHPHADTET 120
DB 79 VDSRRAARQASGPHETITATVGAVTSLQQLAHMRARTHAPYGPYPVPVGYHHPHADTET 138
QY 121 PAQPPRYPAKAVYLPPIPPHIAFPGLSGAVPPSPYPPVAVTGPAPPLHQPSPAHAPPP 180
DB 139 PAQPPRYPAEAVYLPPIPPHIAFPGLSGAVPPSPYPPVAVTGPAPPLHQPSPAHAPPP 198
QY 181 PPPGTPPPPAASLPQEPAGAGALVNASSAAHV 224
DB 199 PPPGTPPPPAASLPQEPAGAGALVNASSAAHV 242
RESULT 9
AAW72192
ID AAW72192 standard; protein; 657 AA.
XX
XX AC AAW72192;
XX
XX DT 13-JAN-1999 (first entry)
XX
XX DE HSV-2 strain SB5 Contig ID 15 ORF#27 protein.
XX
XX KW HSV-2 strain SB5; immunological response induction; therapy;

KW antiviral identification; viral protein inhibitor.
XX
XX OS Herpes simplex virus 2.
XX
XX PN WO9820016-A1.
XX
XX PD 14-MAY-1998.
XX
XX PF 31-OCT-1997; 97WO-US020016.
XX
XX PR 04-NOV-1996; 96US-0030279P.
XX
XX PR 09-JUN-1997; 97US-0049018P.
XX
XX PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
XX ESser KM, Chan JY, Dabrowski-Amaral CE, Delvecchio AM, Dillon SB;
PI Leary JJ;
XX
XX WPI: 1998-286847/25.
XX
XX DR N-PSDB; AAV62176.
XX
XX PT Herpes simplex virus type-2 sequences - useful in, e.g. prevention and
PT treatment of infection or inducing immunological response in mammal.
XX
XX PS Claim 10; Page 120; 748pp; English.
XX
XX CC This sequence represents a Herpes simplex virus type-2 (HSV-2) protein
CC sequence of the invention. This sequence was isolated from a HSV-2 strain
CC SB5 (deposited as ATCC VR-2546) DNA fragment designated Contig ID 15.
CC Based on homology, this sequence is a capsid protein p40. The proteins
CC can be used for the treatment or prevention of disease, to induce an
CC immunological response in a mammal or to identify inhibitors, activators
CC or novel antivirals. Antagonists of the proteins can be used to inhibit a
CC viral polypeptide. The DNA sequence or a vector containing it can also be
CC used to induce an immunological response in a mammal
XX
XX SQ Sequence 657 AA;
Query Match 96.1%; Score 1189; DB 2; Length 657;
Best Local Similarity 99.5%; Pred. No. 1e-80;
Matches 214; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 AIAADROAGGLPAAAGDHGIRGSAKRRRHEVEQPEYDCGRDEPDRDFPYPGEARPEPRP 60
DB 405 AIAADROAGGLPAAAGDHGIRGSAKRRRHEVEQPEYDCGRDEPDRDFPYPGEARPEPRP 464
QY 61 VDSRRAARQASGPHETITATVGAVTSLQQLAHMRARTHAPYGPYPVPVGYHHPHADTET 120
DB 465 VDSRRAARQASGPHETITATVGAVTSLQQLAHMRARTHAPYGPYPVPVGYHHPHADTET 524
QY 121 PAQPPRYPAKAVYLPPIPPHIAFPGLSGAVPPSPYPPVAVTGPAPPLHQPSPAHAPPP 180
DB 525 PAQPPRYPAEAVYLPPIPPHIAFPGLSGAVPPSPYPPVAVTGPAPPLHQPSPAHAPPP 584
QY 181 PPPGTPPPPAASLPQEPAGAGALVNASSAAHV 215
DB 585 PPPGTPPPPAASLPQEPAGAGALVNASSAAHV 619
RESULT 10
AAW71031
ID AAW71031 standard; protein; 635 AA.
XX
XX AC AAW71031;
XX
XX DT 25-MAR-2003 (revised)
XX
XX DT 02-OCT-1995 (first entry)
XX
XX DE HSV-1 UL26 gene product.
XX
XX KW Herpes simplex virus; HSV-1 protease; capsid.
XX
XX OS Herpes simplex virus type 1.

```

XX PN WO9506055-A1.
XX PD 02-MAR-1995.
XX PR 19-AUG-1994; 94WO-US009303.
XX PR 20-AUG-1993; 93US-00110522.
XX PR 23-JUN-1994; 94US-00264537.
XX PA (SMIK ) SMITHLINE BEECHAM CORP.
XX PI Dillella AG, Debouck CM;
XX PR WPI; 1995-106803/14.
XX DR N-PSDB; AAQ84678.
XX PT New herpes simplex virus (HSV)-2 protease and capsid protein - used to
XX PT develop prods. for use in the diagnosis and treatment of HSV-2
XX PT infections.
XX PR Disclosure; Page 35; 51pp; English.
XX PS The sequence is that of a herpes simplex virus type 1 protease and
XX CC capsid. The protein can be used in the diagnosis and treatment of HSV-1
XX CC infections. See also R717017-30. (Updated on 25-MAR-2003 to correct FN
XX CC field.)
XX SQ Sequence 635 AA;
Query Match 54.2%; Score 670.5; DB 2; Length 635;
Best Local Similarity 63.4%; Pred. No. 5.7e-42;
Matches 144; Conservative 12; Mismatches 64; Indels 7; Gaps 4;
QY 1 AIAADROAGGLPAAAGDHGIRGSAKRREHEVEQPEYDCGRDEPRDPFPYVPGEARPPRP 60
DB 403 AIAADROAGGQP--AAGDPGVRGSKRRRYEAGPSESVCDDQDEPDADYPYVPGARGAPRG 461
QY 61 VDSRRARQASGPHETITLAVGAVTSIQQLAHMRARTHAPYGPYPVPGYHHPHADTE- 119
DB 462 VDSRRARHSPGTNETITLAVGAVTSIQQLAHMRARTSAPYGMYPVAHYRQVGSPEP 521
QY 120 TPAQPPRYPAKAVYLPHPHAPPGPLSGA--VPPPSYPVAVTPGAPPLHOPSPAHAH 177
DB 522 TTHPALCPPEAVTRPPHAGPYGPGPASHAPTTPPYAPACPPGPPP---PCPSTQT 578
QY 178 PPPPPGPTPPPAASLPQPEAPGAEGALYNASSAAHVNDTARAAD 224
DB 579 RAPLPTPEAFPFAATGSPASNAEAGALYNASSAAHVVDVTARAAD 625
RESULT 11
ADL18166
XX ID ADL18166 standard; protein; 635 AA.
XX AC ADL18166;
XX XX
XX XX 06-MAY-2004 (first entry)
XX XX Human herpesvirus 1 protease protein SEQ ID NO:86.
XX DE chimeric protein; signal protein; trafficking signal targeting;
XX KW proteolytic cleavage site; protease; protease inhibitor; enzyme.
XX OS Human herpesvirus 1.
XX XX
XX XX WO2003014381-A1.
XX XX
XX PD 20-FEB-2003.
XX PF
XX XX 08-AUG-2002; 2002WO-KR001515.
XX XX
XX PR 10-AUG-2001; 2001KR-00048123.
XX

```

```

XX PA (AHRA-) AHRAH BIOSYSTEMS INC.
XX PI Hwang I, Kim DH, Lee YJ;
XX DR WPI; 2003-256596/25.
XX DR N-PSDB; ADL18165.
XX PT New chimeric protein, useful for detecting protease inhibitors inside the
XX PT cell or tissue.
XX PS Disclosure; SEQ ID NO 86; 214pp; English.
XX CC The present invention describes a chimeric protein comprising at least
XX CC one signal protein that has a trafficking signal targeting to a
XX CC subcellular organelle and at least one proteolytic cleavage site for a
XX CC protease. The chimeric protein is constructed, so that: (a) the
XX CC trafficking signals of all the signal proteins are inactivated by linking
XX CC the proteolytic site or a signal masking protein through the proteolytic
XX CC site to the N-or C- terminus of the signal proteins, and so the chimeric
XX CC protein is present in cytosol; (b) the trafficking signal of at least one
XX CC signal protein is activated when the proteolytic cleavage site is cleaved
XX CC by the protease, and as a result at least one fragment protein that
XX CC includes the activated signal protein is a transported to a subcellular
XX CC organelle; and (c) the chimeric protein is labelled with at least one
XX CC fluorescent protein and the position and intensity distribution of the
XX CC fluorescent label signal in the cell is altered depending on the cleavage
XX CC by the protease. Also described: (1) a recombinant gene comprising a
XX CC nucleic acid sequence encoding the chimeric protein which is constructed
XX CC to express the chimeric protein in a cell; (2) a cell transformed with
XX CC the recombinant gene or vector; (3) analysing the activity of a protease
XX CC in vivo; (4) screening protease inhibitors in vivo; (5) a system for
XX CC detecting a protease inside a cell; (6) a nucleic acid comprising the
XX CC sequence encoding the chimeric protein for detecting protease activity in
XX CC a cell; (7) a vector comprising the nucleic acid; (8) a kit for detecting
XX CC a protease inside a cell comprising the chimeric protein or the vector;
XX CC (9) detecting a protease inside a cell or tissue; and (10) detecting a
XX CC protease inhibitor in vivo. The chimeric protein is useful for detecting
XX CC protease inhibitors inside the cell or tissue. The present sequence
XX CC represents HSV-1 protease, which is used in the exemplification of the
XX CC present invention.
XX SQ Sequence 635 AA;
Query Match 54.2%; Score 670.5; DB 7; Length 635;
Best Local Similarity 63.4%; Pred. No. 5.7e-42;
Matches 144; Conservative 12; Mismatches 64; Indels 7; Gaps 4;
QY 1 AIAADROAGGLPAAAGDHGIRGSAKRREHEVEQPEYDCGRDEPRDPFPYVPGEARPPRP 60
DB 403 AIAADROAGGQP--AAGDPGVRGSKRRRYEAGPSESVCDDQDEPDADYPYVPGARGAPRG 461
QY 61 VDSRRARQASGPHETITLAVGAVTSIQQLAHMRARTHAPYGPYPVPGYHHPHADTE- 119
DB 462 VDSRRARHSPGTNETITLAVGAVTSIQQLAHMRARTSAPYGMYPVAHYRQVGSPEP 521
QY 120 TPAQPPRYPAKAVYLPHPHAPPGPLSGA--VPPPSYPVAVTPGAPPLHOPSPAHAH 177
DB 522 TTHPALCPPEAVTRPPHAGPYGPGPASHAPTTPPYAPACPPGPPP---PCPSTQT 578
QY 178 PPPPPGPTPPPAASLPQPEAPGAEGALYNASSAAHVNDTARAAD 224
DB 579 RAPLPTPEAFPFAATGSPASNAEAGALYNASSAAHVVDVTARAAD 625
RESULT 12
AAR28638
XX ID AAR28638 standard; protein; 415 AA.
XX AC AAR28638;
XX XX
XX XX 25-MAR-2003 (revised)
XX DT 24-MAR-1993 (first entry)

```

```

XX UL26 protease deletion mutant D, amino acids 1-220 deleted.
DE
XX
XX UL26; open reading frame; ORF; protease; herpes simplex virus; HSV;
KW capsid protein; ICP35; ICP35 c; ICP35 d; ICP35 e; ICP35 f;
KW functional domain; insertion; deletion; substitution.
XX
XX Herpes simplex virus type 1.
OS
XX
XX EP514830-A2.
XX
XX 25-NOV-1992.
XX
XX 19-MAY-1992; 92EP-00108420.
XX
XX 24-MAY-1991; 91US-00705814.
XX
XX 07-FEB-1992; 92US-00832855.
XX
XX (ARCH-) ARCH DEV CORP.
XX
XX Roizman B, Liu F;
XX
XX WPI; 1992-391444/48.
XX
XX New herpes serine proteases and corresp. nucleic acid sequences - for
PT detection, prevention and treatment of infection caused by HSV, Epstein-
PT Barr, Varicella-Zoster and CMV cytomegalo-virus.
XX
XX Disclosure; Table 1; 66pp; English.
XX
XX The sequences given in AAR28635-52 are mutants of the protease encoded by
CC the UL26 open reading frame (ORF). The UL26 ORF is contained within a
CC section of the herpes simplex virus (HSV) type 1 genome for the family of
CC HSV capsid proteins designated ICP35. The UL26 transcription initiation
CC site is used as the start point for measurements of distance in this
CC section of the genome. The UL26 protease and ICP35 precursor proteins,
CC ICP35 c and d, may be cleaved by the UL26 protease. Cleavage of ICP35 c
CC and d gives ICP35 e and f respectively. Cleavage specificity of the UL26
CC protease is altered by the inclusion of these mutations. These mutations
CC include insertions, deletions or substitutions which affect the functional
CC domains of the protease. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 415 AA;
SQ
Query Match 53.9%; Score 666.5; DB 2; Length 415;
Best Local Similarity 63.0%; Pred. No. 7.5e-42;
Matches 143; Conservative 12; Mismatches 65; Indels 7; Gaps 4;
QY 1 AIAADROAGGLPAAAGDHGIRGSAKRHRHEVEQPEYDCGRDEPDRDFPYPFGEARPEPRP 60
DB 183 AIAADROAGGQP-AAGDPGVRGSGKRRYEAGPSESICYDQDEPDADYPYPFGEARGAPRG 241
QY 61 VDSRRAARQASGPHTTITALVGAVTSLOQELAHMARTHAPYGPYPVPVGHHPHADTE- 119
DB 242 VDSRRAARHSPTNETITATLMGAVTSLOQELAHMARTSAPYGMTTPVAHYRPQVGEPEP 301
QY 120 TPAQPRPRPAKAVYLPPIHAPPGPLS--GAVPPSPYPVAVTGPAPPLHQPSPAH 177
DB 302 TTTTHALCPPEAVYRPPPHSAPYGPQPPSHAPTPPYAPACPGPPPP---PCPSTQT 358
QY 178 PPPPPPGTTPPAAASLPQEPAGAGALVNASSAAHNVNDTARAAD 224
DB 359 RAPLPTPEAFPPAATGSPQPEASNAEAGALVNASSAAHNVNDTARAAD 405
RESULT 13
AAR28641
ID AAR28641 standard; protein; 603 AA.
XX
XX AAR28641;
XX
XX 25-MAR-2003 (revised)
XX 24-MAR-1993 (first entry)
XX
XX UL26 protease deletion mutant FF, amino acids 1-32 deleted.
DE
XX
XX UL26; open reading frame; ORF; protease; herpes simplex virus; HSV;
KW capsid protein; ICP35; ICP35 c; ICP35 d; ICP35 e; ICP35 f;
KW functional domain; insertion; deletion; substitution.
XX
XX Herpes simplex virus type 1.
OS
XX
XX EP514830-A2.
XX
XX 25-NOV-1992.
XX
XX 19-MAY-1992; 92EP-00108420.
XX
XX 24-MAY-1991; 91US-00705814.
XX
XX 07-FEB-1992; 92US-00832855.
XX
XX (ARCH-) ARCH DEV CORP.
XX
XX Roizman B, Liu F;
XX
XX WPI; 1992-391444/48.
XX
XX New herpes serine proteases and corresp. nucleic acid sequences - for
PT detection, prevention and treatment of infection caused by HSV, Epstein-
PT Barr, Varicella-Zoster and CMV cytomegalo-virus.
XX
XX Disclosure; Table 1; 66pp; English.
XX
XX The sequences given in AAR28635-52 are mutants of the protease encoded by
CC the UL26 open reading frame (ORF). The UL26 ORF is contained within a
CC section of the herpes simplex virus (HSV) type 1 genome for the family of
CC HSV capsid proteins designated ICP35. The UL26 transcription initiation
CC site is used as the start point for measurements of distance in this
CC section of the genome. The UL26 protease and ICP35 precursor proteins,
CC ICP35 c and d, may be cleaved by the UL26 protease. Cleavage of ICP35 c
CC and d gives ICP35 e and f respectively. Cleavage specificity of the UL26
CC protease is altered by the inclusion of these mutations. These mutations
CC include insertions, deletions or substitutions which affect the functional
CC domains of the protease. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 603 AA;
SQ
Query Match 53.9%; Score 666.5; DB 2; Length 603;
Best Local Similarity 63.0%; Pred. No. 1.1e-41;
Matches 143; Conservative 12; Mismatches 65; Indels 7; Gaps 4;
QY 1 AIAADROAGGLPAAAGDHGIRGSAKRHRHEVEQPEYDCGRDEPDRDFPYPFGEARPEPRP 60
DB 371 AIAADROAGGQP-AAGDPGVRGSGKRRYEAGPSESICYDQDEPDADYPYPFGEARGAPRG 429
QY 61 VDSRRAARQASGPHTTITALVGAVTSLOQELAHMARTHAPYGPYPVPVGHHPHADTE- 119
DB 430 VDSRRAARHSPTNETITATLMGAVTSLOQELAHMARTSAPYGMTTPVAHYRPQVGEPEP 489
QY 120 TPAQPRPRPAKAVYLPPIHAPPGPLS--GAVPPSPYPVAVTGPAPPLHQPSPAH 177
DB 490 TTTTHALCPPEAVYRPPPHSAPYGPQPPSHAPTPPYAPACPGPPPP---PCPSTQT 546
QY 178 PPPPPPGTTPPAAASLPQEPAGAGALVNASSAAHNVNDTARAAD 224
DB 547 RAPLPTPEAFPPAATGSPQPEASNAEAGALVNASSAAHNVNDTARAAD 593
RESULT 14
AAR28640
ID AAR28640 standard; protein; 626 AA.
XX
XX AAR28640;
XX
XX 25-MAR-2003 (revised)
XX 24-MAR-1993 (first entry)
XX

```

XX UL26 protease deletion mutant EE, amino acids 1-9 deleted.

DE

XX

KW UL26; open reading frame; ORF; protease; herpes simplex virus; HSV;

KW capsid protein; ICP35 c; ICP35 d; ICP35 e; ICP35 f;

KW functional domain; insertion; deletion; substitution.

OS

XX Herpes simplex virus type 1.

XX

PN EP514830-A2.

XX

PD 25-NOV-1992.

XX

XX

PF 19-MAY-1992; 92EP-00108420.

XX

PR 24-MAY-1991; 91US-00705814.

PR

07-FEB-1992; 92US-00832855.

XX

XX (ARCH-) ARCH DEV CORP.

PA

XX Roizman B, Liu F;

PI

XX WPI; 1992-391444/48.

DR

XX

XX New herpes serine proteases and corresp. nucleic acid sequences - for

PT detection, prevention and treatment of infection caused by HSV, Epstein-

PT Barr, Varicella-Zoster and CMV cytomegalo-virus.

XX

XX Disclosure; Table 1; 66pp; English.

PS

XX

XX The sequences given in AAR28635-52 are mutants of the protease encoded by

CC the UL26 open reading frame (ORF). The UL26 ORF is contained within a

CC section of the herpes simplex virus (HSV) type 1 genome for the family of

CC HSV capsid proteins designated ICP35. The UL26 transcription initiation

CC site is used as the start point for measurements of distance in this

CC section of the genome. The UL26 protease and ICP35 precursor proteins,

CC ICP35 c and d, may be cleaved by the UL26 protease. Cleavage of ICP35 c

CC and d gives ICP35 e and f respectively. Cleavage specificity of the UL26

CC protease is altered by the inclusion of these mutations. These mutations

CC include insertions, deletions or substitutions which affect the functional

CC domains of the protease. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 626 AA;

Query Match 53.9%; Score 666.5; DB 2; Length 626;

Best Local Similarity 63.0%; Pred. No. 1.1e-41;

Matches 143; Conservative 12; Mismatches 65; Indels 7; Gaps 4;

QY 1 AIAADROAGGLPAAAGDHGIRGSAKRRRHEVEQPEYDCGRDEPRDPFPYYPGEARPEPRP 60

DB 394 AIAADROAGQP-AAGDPGVRGSGKRRRYEAGSPSEYCDQDEPDADYPYYPGEARGAPRG 452

QY 61 VDSRRRAQASGPHETITLAVGAVTSIQQLAHMRARTHAPYGPYPVPVGYHHPHADTE- 119

DB 453 VDSRRRAHSPGNETITLGMGAVTSIQQLAHMRARTSAPYGMVTFVAHYRQVGEPEP 512

QY 120 TPAQPRYPYPAKAVYLPPIPHIAPPGLPLS--GAVPPPSYPVAVTPGAPPLHQPSPAHAH 177

DB 513 TTHPALCPPEAVYRPPHSAFYGPQGPSPHAPTTPYAPACCPGPPPP--PCPSTQT 569

QY 178 PPPPPGPTPPPAASLPQPEAPGAEAGALVNASSAAHVNDVTARAAD 224

DB 570 RAPLPTPEAPPAPPAATGSQPEASNAEAGALVNASSAAHVNDVTARAAD 616

RESULT 15

AAR28634

ID AAR28634 standard; protein; 635 AA.

XX

AC AAR28634;

XX

DT 25-MAR-2003 (revised)

DT 24-MAR-1993 (first entry)

XX UL26 protease.

DE

XX

KW UL26; open reading frame; ORF; protease; herpes simplex virus; HSV;

KW capsid protein; ICP35 c; ICP35 d; ICP35 e; ICP35 f;

KW functional domain.

OS

XX Herpes simplex virus type 1.

XX

PN EP514830-A2.

XX

PD 25-NOV-1992.

XX

XX

PF 19-MAY-1992; 92EP-00108420.

XX

PR 24-MAY-1991; 91US-00705814.

PR

07-FEB-1992; 92US-00832855.

XX

XX (ARCH-) ARCH DEV CORP.

PA

XX Roizman B, Liu F;

PI

XX WPI; 1992-391444/48.

DR

XX

XX N-PSDB; AAQ30736.

DR

XX

XX New herpes serine proteases and corresp. nucleic acid sequences - for

PT detection, prevention and treatment of infection caused by HSV, Epstein-

PT Barr, Varicella-Zoster and CMV cytomegalo-virus.

XX

XX Disclosure; Fig 1B; 66pp; English.

PS

XX

XX This sequence is encoded by the UL26 open reading frame (ORF) and it is a

CC protease. The UL26 ORF is contained within a section of the herpes

CC simplex virus (HSV) type 1 genome for the family of HSV capsid proteins

CC designated ICP35. The UL26 transcription initiation site is used as the

CC start point for measurements of distance in this section of the genome.

CC The UL26 protease and ICP35 precursor proteins, ICP35 c and d, may be

CC cleaved by the UL26 protease. Cleavage of ICP35 c and d gives ICP35 e and

CC f respectively. Cleavage specificity of the UL26 protease may be altered

CC by mutations within the sequence. These mutations may be insertions,

CC deletions or substitutions which affect the functional domains of the

CC protease. See also AAR28635-52. (Updated on 25-MAR-2003 to correct PN

CC field.)

XX

SQ Sequence 635 AA;

Query Match 53.9%; Score 666.5; DB 2; Length 635;

Best Local Similarity 63.0%; Pred. No. 1.1e-41;

Matches 143; Conservative 12; Mismatches 65; Indels 7; Gaps 4;

QY 1 AIAADROAGGLPAAAGDHGIRGSAKRRRHEVEQPEYDCGRDEPRDPFPYYPGEARPEPRP 60

DB 403 AIAADROAGQP-AAGDPGVRGSGKRRRYEAGSPSEYCDQDEPDADYPYYPGEARGAPRG 461

QY 61 VDSRRRAQASGPHETITLAVGAVTSIQQLAHMRARTHAPYGPYPVPVGYHHPHADTE- 119

DB 462 VDSRRRAHSPGNETITLGMGAVTSIQQLAHMRARTSAPYGMVTFVAHYRQVGEPEP 521

QY 120 TPAQPRYPYPAKAVYLPPIPHIAPPGLPLS--GAVPPPSYPVAVTPGAPPLHQPSPAHAH 177

DB 522 TTHPALCPPEAVYRPPHSAFYGPQGPSPHAPTTPYAPACCPGPPPP--PCPSTQT 578

QY 178 PPPPPGPTPPPAASLPQPEAPGAEAGALVNASSAAHVNDVTARAAD 224

DB 579 RAPLPTPEAPPAPPAATGSQPEASNAEAGALVNASSAAHVNDVTARAAD 625

Search completed: July 27, 2005, 12:18:38

Job time : 167 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 27, 2005, 12:31:33 ; Search time 39 Seconds
(without alignments)
22.204 Million cell updates/sec

Title: US-10-623-429-9_COPY_475_483
Perfect score: 48
Sequence: 1 GPHETITAL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|--------------------|
| 1 | 38 | 79.2 | 83 | 2 S24712 | Ig alpha chain - h |
| 2 | 37 | 77.1 | 404 | 2 T35421 | probable regulator |
| 3 | 36 | 75.0 | 459 | 2 E86726 | cell division prot |
| 4 | 36 | 75.0 | 1825 | 2 C88400 | protein H19W22.1 l |
| 5 | 36 | 75.0 | 1825 | 2 T32828 | hypothetical prote |
| 6 | 35 | 72.9 | 201 | 2 A12205 | hypothetical prote |
| 7 | 35 | 72.9 | 334 | 2 AB0936 | N-acetyl-gamma-glu |
| 8 | 35 | 72.9 | 515 | 1 T06595 | 2-amino-4-hydroxy- |
| 9 | 35 | 72.9 | 724 | 2 B71404 | hypothetical prote |
| 10 | 35 | 72.9 | 1239 | 1 VHWVEE | structural polypro |
| 11 | 35 | 72.9 | 1240 | 1 VHWVEV | structural polypro |
| 12 | 35 | 72.9 | 1241 | 2 S26373 | genome polyprotein |
| 13 | 35 | 72.9 | 1242 | 2 A56605 | structural polypro |
| 14 | 35 | 72.9 | 1242 | 2 S72350 | structural polypro |
| 15 | 35 | 72.9 | 1324 | 2 T14070 | peptide synthetase |
| 16 | 34 | 70.8 | 143 | 2 A70573 | hypothetical prote |
| 17 | 34 | 70.8 | 478 | 2 T40860 | probable alpha-amy |
| 18 | 34 | 70.8 | 653 | 2 G82971 | probable ferredoxi |
| 19 | 33 | 68.8 | 181 | 2 D87196 | probable membrane |
| 20 | 33 | 68.8 | 259 | 2 C70530 | hypothetical prote |
| 21 | 33 | 68.8 | 384 | 2 AD0049 | hypothetical prote |
| 22 | 33 | 68.8 | 418 | 2 E69014 | hypothetical prote |
| 23 | 33 | 68.8 | 511 | 2 D69671 | phosphoglycerate m |
| 24 | 33 | 68.8 | 557 | 2 E86106 | yidB protein [semi |
| 25 | 33 | 68.8 | 557 | 2 S56342 | yidB protein - Esc |
| 26 | 33 | 68.8 | 557 | 2 H91265 | hypothetical prote |
| 27 | 33 | 68.8 | 613 | 2 D87380 | hypothetical prote |
| 28 | 33 | 68.8 | 633 | 2 S49788 | probable membrane |
| 29 | 33 | 68.8 | 635 | 1 WNBEM6 | capsid protein - h |

| | | | | | |
|-----|------|------|---|--------|---------------------|
| 30 | 68.8 | 706 | 2 | D82452 | anaerobic ribonucel |
| 31 | 68.8 | 707 | 1 | A64047 | ribonucleoside-tri |
| 32 | 68.8 | 712 | 1 | A47331 | ribonucleoside-tri |
| 33 | 68.8 | 712 | 2 | AC1058 | ribonucleoside-tri |
| 34 | 68.8 | 712 | 2 | G91280 | anaerobic ribonucel |
| 35 | 68.8 | 712 | 2 | G86121 | anaerobic ribonucel |
| 36 | 68.8 | 712 | 2 | AG0419 | ribonucleoside-tri |
| 37 | 68.8 | 971 | 2 | S54595 | probable membrane |
| 38 | 68.8 | 1008 | 2 | T30544 | major surface glyco |
| 39 | 68.8 | 1017 | 2 | T30542 | major surface glyco |
| 40 | 68.8 | 1022 | 2 | T30543 | major surface glyco |
| 41 | 68.8 | 1179 | 2 | C36792 | hypothetical prote |
| 42 | 68.8 | 1267 | 1 | MXR31 | lambda 3 protein - |
| 43 | 68.8 | 1267 | 1 | MXR32 | lambda 3 protein - |
| 44 | 68.8 | 1267 | 1 | MXR33 | lambda 3 protein - |
| 45 | 67.7 | 467 | 2 | T38353 | serine hydroxymeth |
| 46 | 67.7 | 472 | 2 | T37918 | serine hydroxymeth |
| 47 | 67.7 | 479 | 1 | A42241 | glycine hydroxymet |
| 48 | 66.7 | 117 | 2 | T03782 | probable lipid tra |
| 49 | 66.7 | 118 | 2 | T02042 | lipid transfer pro |
| 50 | 66.7 | 118 | 2 | T03300 | probable lipid tra |
| 51 | 66.7 | 141 | 2 | H75583 | probable copper re |
| 52 | 66.7 | 168 | 2 | B69199 | hypothetical prote |
| 53 | 66.7 | 179 | 2 | C70507 | hypothetical prote |
| 54 | 66.7 | 343 | 2 | C90435 | hypothetical prote |
| 55 | 66.7 | 404 | 2 | E83851 | N-acyl-L-amino aci |
| 56 | 66.7 | 425 | 2 | B88012 | cell division prot |
| 57 | 66.7 | 429 | 2 | D95144 | hypothetical prote |
| 58 | 66.7 | 466 | 2 | PC4296 | nicotinic acetylch |
| 59 | 66.7 | 479 | 2 | D70641 | hypothetical prote |
| 60 | 66.7 | 554 | 2 | T08976 | 2-amino-4-hydroxy- |
| 61 | 66.7 | 579 | 2 | B44857 | acetylactate synth |
| 62 | 66.7 | 680 | 2 | T03106 | probable transport |
| 63 | 66.7 | 680 | 2 | T08080 | probable myrosinas |
| 64 | 66.7 | 858 | 2 | E72419 | flagellar hook-ass |
| 65 | 66.7 | 912 | 2 | T18785 | hypothetical prote |
| 66 | 66.7 | 1213 | 2 | T37959 | hypothetical prote |
| 67 | 66.7 | 2035 | 2 | AC0233 | yersiniabactin bio |
| 68 | 66.7 | 2035 | 2 | A48654 | probable polyketid |
| 69 | 66.7 | 2041 | 2 | T17439 | peptide synthetase |
| 70 | 66.7 | 29 | 2 | S34762 | L-serine ammonia-1 |
| 71 | 64.6 | 98 | 2 | D95371 | hypothetical prote |
| 72 | 64.6 | 132 | 2 | G82805 | two-component syst |
| 73 | 64.6 | 139 | 2 | S03485 | r-cell receptor be |
| 74 | 64.6 | 201 | 2 | T24183 | hypothetical prote |
| 75 | 64.6 | 261 | 2 | C84366 | probable oxidoredu |
| 76 | 64.6 | 315 | 2 | H86836 | carbamate kinase (|
| 77 | 64.6 | 327 | 2 | T44432 | fatty acid/phospho |
| 78 | 64.6 | 339 | 2 | E71518 | uroporphyrinogen d |
| 79 | 64.6 | 340 | 2 | D64595 | uroporphyrinogen d |
| 80 | 64.6 | 351 | 1 | A55962 | opsin, pineal glan |
| 81 | 64.6 | 370 | 2 | I40358 | N-acyl-L-amino aci |
| 82 | 64.6 | 370 | 2 | JC6130 | paired box transcr |
| 83 | 64.6 | 374 | 2 | F69233 | carbamoyl-phosphat |
| 84 | 64.6 | 401 | 2 | D83618 | beta-ketoadipyl Co |
| 85 | 64.6 | 422 | 2 | AG1323 | threonine dehydrat |
| 86 | 64.6 | 422 | 2 | AH1694 | threonine dehydrat |
| 87 | 64.6 | 434 | 2 | AG1040 | Vi polysaccharide |
| 88 | 64.6 | 434 | 2 | I36892 | Vi polysaccharide |
| 89 | 64.6 | 435 | 2 | T35884 | tagatose 6-phospha |
| 90 | 64.6 | 455 | 2 | B70664 | hypothetical prote |
| 91 | 64.6 | 521 | 2 | S55317 | cytochrome p450 1A |
| 92 | 64.6 | 558 | 2 | T19748 | hypothetical prote |
| 93 | 64.6 | 583 | 1 | JC2545 | acid phosphatase (|
| 94 | 64.6 | 668 | 2 | S56209 | polymyxin B resist |
| 95 | 64.6 | 772 | 2 | S22860 | excision repair pr |
| 96 | 64.6 | 809 | 2 | A55547 | quinolate-shikimate |
| 97 | 64.6 | 964 | 2 | S48404 | probable membrane |
| 98 | 64.6 | 1018 | 2 | JC5799 | alpha-D-mannosidas |
| 99 | 64.6 | 1027 | 2 | I38604 | p53-binding protei |
| 100 | 64.6 | 1039 | 2 | T35878 | hypothetical prote |
| 101 | 64.6 | 1041 | 2 | S42509 | Rag-1 protein - ch |
| 102 | 64.6 | 1042 | 2 | S42511 | Rag-1 protein - ra |

| | | | | | | | | | | | | | |
|-----|------|------|-------|---|--------|----------------------|-----|----|------|-------|---|--------|---------------------|
| 103 | 31 | 64.6 | 1043 | 2 | B33754 | recombination-acti | 176 | 30 | 62.5 | 813 | 2 | S36018 | gene tramtrack-p88 |
| 104 | 31 | 64.6 | 1043 | 2 | A33754 | recombination-acti | 177 | 30 | 62.5 | 923 | 2 | S44226 | periodic tryptophan |
| 105 | 31 | 64.6 | 1045 | 2 | I51555 | recombination acti | 178 | 30 | 62.5 | 941 | 2 | T33032 | hypothetical prote |
| 106 | 31 | 64.6 | 1087 | 2 | F72283 | beta-galactosidase | 179 | 30 | 62.5 | 1157 | 2 | C96761 | hypothetical prote |
| 107 | 31 | 64.6 | 1231 | 2 | S53089 | protein-tyrosine-p | 180 | 30 | 62.5 | 1173 | 2 | T30608 | proteophosphoglyca |
| 108 | 31 | 64.6 | 1254 | 2 | T18277 | kinesin heavy chai | 181 | 30 | 62.5 | 1250 | 2 | T00454 | hypothetical prote |
| 109 | 31 | 64.6 | 1488 | 2 | T02856 | probable membrane | 182 | 30 | 62.5 | 1443 | 2 | T31896 | hypothetical prote |
| 110 | 31 | 64.6 | 1762 | 2 | T03222 | probable polyketid | 183 | 30 | 62.5 | 1587 | 2 | A82012 | hypothetical prote |
| 111 | 31 | 64.6 | 15281 | 2 | S41309 | cyclosporin synthe | 184 | 30 | 62.5 | 1791 | 2 | T02909 | hypothetical prote |
| 112 | 30.5 | 63.5 | 274 | 2 | A84302 | ketopantoate hydro | 185 | 30 | 62.5 | 2318 | 2 | S45306 | notch 3 protein - |
| 113 | 30.5 | 62.5 | 25 | 2 | S22221 | peroxidase (EC 1.1 | 186 | 30 | 62.5 | 3766 | 2 | T29165 | hypothetical prote |
| 114 | 30 | 62.5 | 49 | 2 | E07309 | hypothetical prote | 187 | 30 | 62.5 | 4848 | 2 | T30289 | pristinamycin I sy |
| 115 | 30 | 62.5 | 114 | 2 | E97017 | hypothetical prote | 188 | 30 | 62.5 | 26926 | 1 | I38344 | tiatin, cardiac mus |
| 116 | 30 | 62.5 | 126 | 2 | C90797 | hypothetical prote | 189 | 29 | 60.4 | 99 | 2 | G83295 | hypothetical prote |
| 117 | 30 | 62.5 | 148 | 2 | E87609 | hypothetical prote | 190 | 29 | 60.4 | 116 | 2 | H50614 | NADH dehydrogenase |
| 118 | 30 | 62.5 | 196 | 2 | T10206 | hypothetical prote | 191 | 29 | 60.4 | 122 | 2 | A83427 | transposase BMS114 |
| 119 | 30 | 62.5 | 210 | 2 | D72490 | hypothetical prote | 192 | 29 | 60.4 | 130 | 2 | T48771 | hypothetical prote |
| 120 | 30 | 62.5 | 212 | 2 | B84337 | deoxyribose-phosph | 193 | 29 | 60.4 | 143 | 2 | E69065 | molybdopterin bios |
| 121 | 30 | 62.5 | 225 | 2 | F86417 | hypothetical prote | 194 | 29 | 60.4 | 145 | 2 | D84776 | probable ubiquitin |
| 122 | 30 | 62.5 | 245 | 2 | H97865 | pseudouridylylate sy | 195 | 29 | 60.4 | 146 | 2 | T08443 | probable DNA-bind |
| 123 | 30 | 62.5 | 262 | 1 | FK5SK | kanamycin kinase (| 196 | 29 | 60.4 | 154 | 2 | A10347 | probable exported |
| 124 | 30 | 62.5 | 269 | 2 | D82001 | probable integral | 197 | 29 | 60.4 | 159 | 2 | I40564 | hypothetical DNA-b |
| 125 | 30 | 62.5 | 269 | 2 | G81230 | conserved hypotnet | 198 | 29 | 60.4 | 174 | 1 | WRBP70 | early protein gpi7 |
| 126 | 30 | 62.5 | 281 | 2 | T35932 | probable inositol | 199 | 29 | 60.4 | 174 | 2 | A86192 | hypothetical prote |
| 127 | 30 | 62.5 | 283 | 2 | T15229 | hypothetical prote | 200 | 29 | 60.4 | 182 | 2 | S78137 | cytochrome-c oxida |
| 128 | 30 | 62.5 | 286 | 2 | T25559 | hypothetical prote | 201 | 29 | 60.4 | 184 | 2 | B86192 | hypothetical prote |
| 129 | 30 | 62.5 | 291 | 2 | S78602 | peroxidase (EC 1.1 | 202 | 29 | 60.4 | 198 | 2 | A83424 | regulatory protein |
| 130 | 30 | 62.5 | 296 | 2 | T12469 | hypothetical prote | 203 | 29 | 60.4 | 200 | 2 | C82224 | probable alpha-rib |
| 131 | 30 | 62.5 | 301 | 2 | T37326 | probable transcrip | 204 | 29 | 60.4 | 205 | 2 | C75096 | probable acetyltra |
| 132 | 30 | 62.5 | 313 | 2 | E87705 | hypothetical prote | 205 | 29 | 60.4 | 210 | 1 | JQ0394 | nodB protein - Azo |
| 133 | 30 | 62.5 | 319 | 2 | B69806 | divalent cation tr | 206 | 29 | 60.4 | 221 | 2 | B82647 | hypothetical prote |
| 134 | 30 | 62.5 | 331 | 2 | C97493 | malonyl-CoA-acyl c | 207 | 29 | 60.4 | 234 | 2 | H75390 | hypothetical prote |
| 135 | 30 | 62.5 | 331 | 2 | A82711 | malonyl-CoA-acyl c | 208 | 29 | 60.4 | 240 | 2 | G82295 | conserved hypotnet |
| 136 | 30 | 62.5 | 334 | 1 | RDECEP | N-acetyl-gamma-glu | 209 | 29 | 60.4 | 243 | 2 | T36108 | conserved hypotnet |
| 137 | 30 | 62.5 | 334 | 2 | G91239 | N-acetyl-gamma-glu | 210 | 29 | 60.4 | 245 | 2 | B69118 | modulator recognit |
| 138 | 30 | 62.5 | 334 | 2 | D86087 | N-acetyl-gamma-glu | 211 | 29 | 60.4 | 246 | 2 | S27963 | hypothetical prote |
| 139 | 30 | 62.5 | 351 | 2 | D82930 | SRP family of GTP- | 212 | 29 | 60.4 | 249 | 2 | F84118 | hypothetical prote |
| 140 | 30 | 62.5 | 360 | 2 | C82220 | hypothetical prote | 213 | 29 | 60.4 | 263 | 2 | B87486 | probable regulator |
| 141 | 30 | 62.5 | 363 | 2 | S31780 | peroxidase (EC 1.1 | 214 | 29 | 60.4 | 279 | 2 | A80285 | conserved hypotnet |
| 142 | 30 | 62.5 | 364 | 2 | E81702 | phospholipase D fa | 215 | 29 | 60.4 | 289 | 2 | F69313 | conserved hypotnet |
| 143 | 30 | 62.5 | 371 | 2 | D85606 | hypothetical prote | 216 | 29 | 60.4 | 293 | 1 | B9AG58 | virB9 protein prec |
| 144 | 30 | 62.5 | 389 | 2 | D49776 | hypothetical prote | 217 | 29 | 60.4 | 293 | 2 | A83249 | component of type |
| 145 | 30 | 62.5 | 393 | 2 | AG0091 | probable flagellar | 218 | 29 | 60.4 | 301 | 2 | E71558 | probable fad synth |
| 146 | 30 | 62.5 | 405 | 2 | B47071 | nitrogenase cofact | 219 | 29 | 60.4 | 304 | 2 | T40210 | hypothetical prote |
| 147 | 30 | 62.5 | 404 | 2 | AE0973 | O-antigen ligase l | 220 | 29 | 60.4 | 313 | 2 | A12806 | carbohydrate kinas |
| 148 | 30 | 62.5 | 404 | 2 | B41317 | O-antigen ligase c | 221 | 29 | 60.4 | 313 | 2 | H97585 | carbohydrate kinas |
| 149 | 30 | 62.5 | 405 | 2 | T40193 | hypothetical prote | 222 | 29 | 60.4 | 315 | 2 | H37368 | truD protein (AE00 |
| 150 | 30 | 62.5 | 409 | 2 | F90825 | probable integrase | 223 | 29 | 60.4 | 315 | 2 | AH2586 | tRNA pseudouridine |
| 151 | 30 | 62.5 | 413 | 2 | T48089 | hypothetical prote | 224 | 29 | 60.4 | 317 | 2 | B81667 | ferrochelatase TC0 |
| 152 | 30 | 62.5 | 416 | 2 | A85684 | probable integrase | 225 | 29 | 60.4 | 322 | 2 | H83852 | L-asparaginase BH1 |
| 153 | 30 | 62.5 | 454 | 2 | A82353 | glutathione-disulf | 226 | 29 | 60.4 | 324 | 2 | T34196 | hypothetical prote |
| 154 | 30 | 62.5 | 483 | 2 | S75369 | hypothetical prote | 227 | 29 | 60.4 | 324 | 2 | E84918 | hypothetical prote |
| 155 | 30 | 62.5 | 493 | 2 | C95216 | galactose-1-phosph | 228 | 29 | 60.4 | 325 | 2 | T47229 | arginase (EC 3.5.3 |
| 156 | 30 | 62.5 | 493 | 2 | A98080 | UTP-hexose-1-phosp | 229 | 29 | 60.4 | 329 | 2 | JC4093 | signal recognition |
| 157 | 30 | 62.5 | 497 | 2 | D97264 | galactose-1-phosph | 230 | 29 | 60.4 | 330 | 2 | F83960 | signal recognition |
| 158 | 30 | 62.5 | 497 | 2 | S27785 | acetyl-CoA acetyl | 231 | 29 | 60.4 | 330 | 2 | H95166 | transcription regu |
| 159 | 30 | 62.5 | 508 | 2 | E83788 | galactose-1-phosph | 232 | 29 | 60.4 | 330 | 2 | G98032 | hypothetical prote |
| 160 | 30 | 62.5 | 517 | 2 | T05620 | glycine hydroxymet | 233 | 29 | 60.4 | 340 | 2 | S75099 | hypothetical prote |
| 161 | 30 | 62.5 | 518 | 1 | S40218 | glycine hydroxymet | 234 | 29 | 60.4 | 346 | 2 | C30754 | hypothetical prote |
| 162 | 30 | 62.5 | 530 | 2 | A45690 | transactivator EBN | 235 | 29 | 60.4 | 352 | 2 | T36332 | hypothetical prote |
| 163 | 30 | 62.5 | 532 | 2 | T01759 | glycine hydroxymet | 236 | 29 | 60.4 | 357 | 2 | T20659 | hypothetical prote |
| 164 | 30 | 62.5 | 553 | 2 | S77623 | mannuronan C-5-epi | 237 | 29 | 60.4 | 358 | 2 | T47228 | arginase (EC 3.5.3 |
| 165 | 30 | 62.5 | 561 | 2 | G84012 | oligo-1,6-glucosid | 238 | 29 | 60.4 | 358 | 2 | B64427 | carbamoyl-phosphat |
| 166 | 30 | 62.5 | 577 | 2 | T18116 | hypothetical prote | 239 | 29 | 60.4 | 365 | 2 | S56792 | hypothetical prote |
| 167 | 30 | 62.5 | 599 | 2 | H72454 | probable fatty-aci | 240 | 29 | 60.4 | 365 | 2 | F88449 | protein F54D8.4 li |
| 168 | 30 | 62.5 | 637 | 2 | H71254 | probable DNA gyrase | 241 | 29 | 60.4 | 368 | 2 | A11291 | glycerol dehydroge |
| 169 | 30 | 62.5 | 638 | 2 | JC7753 | ring finger B-box | 242 | 29 | 60.4 | 368 | 2 | AG1663 | glycerol dehydroge |
| 170 | 30 | 62.5 | 640 | 2 | F90364 | hypothetical prote | 243 | 29 | 60.4 | 368 | 2 | S75923 | sensory transducti |
| 171 | 30 | 62.5 | 642 | 2 | S44542 | probable membrane | 244 | 29 | 60.4 | 382 | 2 | A70705 | probable PE protei |
| 172 | 30 | 62.5 | 648 | 1 | DJBPS2 | DNA-directed DNA p | 245 | 29 | 60.4 | 385 | 2 | E82317 | D-erythrose 4-phos |
| 173 | 30 | 62.5 | 655 | 2 | T07090 | probable priA prot | 246 | 29 | 60.4 | 391 | 2 | G89822 | hypothetical prote |
| 174 | 30 | 62.5 | 718 | 2 | A13420 | penicillin-binding | 247 | 29 | 60.4 | 393 | 2 | H90291 | thermostable carbo |
| 175 | 30 | 62.5 | 739 | 1 | VHIWEB | nucleocapsid prote | 248 | 29 | 60.4 | 393 | 2 | A9361 | thermostable carbo |

249 29 60.4 393 2 S76696
250 29 60.4 393 2 AC1142
251 29 60.4 393 2 AF1500
252 29 60.4 393 2 T49578
253 29 60.4 394 2 S62726
254 29 60.4 405 2 G86848
255 29 60.4 424 2 T40641
256 29 60.4 426 2 H65102
257 29 60.4 426 2 B85130
258 29 60.4 426 2 B85975
259 29 60.4 441 2 AH2068
260 29 60.4 449 2 A44989
261 29 60.4 449 2 A30303
262 29 60.4 455 1 T15581
263 29 60.4 459 2 F71131
264 29 60.4 462 2 G70015
265 29 60.4 464 2 G70362
266 29 60.4 468 2 C82722
267 29 60.4 487 2 S61243
268 29 60.4 487 2 A87434
269 29 60.4 491 2 A24814
270 29 60.4 491 2 A31418
271 29 60.4 491 2 JC5312
272 29 60.4 491 2 E95213
273 29 60.4 491 2 F98077
274 29 60.4 508 2 H75605
275 29 60.4 513 2 T45624
276 29 60.4 513 2 S39691
277 29 60.4 521 2 A29345
278 29 60.4 543 2 T06523
279 29 60.4 556 2 G86319
280 29 60.4 558 2 D69067
281 29 60.4 568 2 S19031
282 29 60.4 577 2 B75621
283 29 60.4 590 2 T11098
284 29 60.4 622 2 T27155
285 29 60.4 624 2 T01585
286 29 60.4 641 2 A42019
287 29 60.4 651 2 S24609
288 29 60.4 665 1 T44793
289 29 60.4 684 2 T47694
290 29 60.4 693 2 JN0673
291 29 60.4 700 2 D70951
292 29 60.4 701 2 JN0674
293 29 60.4 733 2 A57459
294 29 60.4 770 2 S04847
295 29 60.4 776 2 AH1506
296 29 60.4 788 2 AB1991
297 29 60.4 867 2 T00118
298 29 60.4 878 2 C71305
299 29 60.4 980 2 E86589
300 29 60.4 980 2 E72035
301 29 60.4 1102 2 A84480
302 29 60.4 1148 2 D85360
303 29 60.4 1209 2 E90994
304 29 60.4 1209 2 H85839
305 29 60.4 1210 2 E64979
306 29 60.4 1243 2 T17390
307 29 60.4 1246 2 JQ0406
308 29 60.4 1254 1 JQ1979
309 29 60.4 1254 1 VHWVVE
310 29 60.4 1254 1 VHWVVT
311 29 60.4 1255 1 B44213
312 29 60.4 1255 1 D42133
313 29 60.4 1282 2 JE0120
314 29 60.4 1283 2 T39174
315 29 60.4 1307 2 T30887
316 29 60.4 1322 2 T24140
317 29 60.4 1354 2 T13930
318 29 60.4 1364 2 T00250
319 29 60.4 1466 2 G84516
320 29 60.4 1506 2 S52957
321 29 60.4 1974 2 T16703

322 29 60.4 2204 1 RRNZV
323 29 60.4 2278 1 S56274
324 29 60.4 2403 2 T30875
325 29 60.4 3172 2 S22012
326 29 60.4 3178 2 S13595
327 29 60.4 3588 2 I40485
328 29 60.4 4485 2 T08044
329 29 60.4 9376 2 T14593
330 28.5 59.4 256 2 AH1978
331 28.5 59.4 517 2 S40212
332 28.5 59.4 517 2 S40213
333 28.5 59.4 518 1 A42906
334 28.5 59.4 2257 2 T34918
335 28 58.3 27 4 I52725
336 28 58.3 70 2 AG0345
337 28 58.3 72 2 JC1474
338 28 58.3 77 2 C72808
339 28 58.3 86 2 S36533
340 28 58.3 112 2 S77344
341 28 58.3 113 2 C69818
342 28 58.3 113 2 D84389
343 28 58.3 135 2 F72688
344 28 58.3 148 2 AG2200
345 28 58.3 151 2 A39392
346 28 58.3 154 2 E84275
347 28 58.3 179 2 S23358
348 28 58.3 181 2 AG1764
349 28 58.3 190 2 T21878
350 28 58.3 191 2 A82613
351 28 58.3 192 2 T35904
352 28 58.3 202 2 S59955
353 28 58.3 204 2 G95017
354 28 58.3 204 2 H70780
355 28 58.3 211 2 E70045
356 28 58.3 211 2 T35272
357 28 58.3 217 2 T37832
358 28 58.3 217 2 T03496
359 28 58.3 219 2 S56810
360 28 58.3 221 2 H70395
361 28 58.3 226 2 JQ2121
362 28 58.3 226 2 T27286
363 28 58.3 227 2 G83724
364 28 58.3 227 2 F86840
365 28 58.3 230 2 T11290
366 28 58.3 230 2 D14586
367 28 58.3 232 2 D95113
368 28 58.3 237 2 C97982
369 28 58.3 237 2 D71287
370 28 58.3 238 2 H84330
371 28 58.3 239 2 E84232
372 28 58.3 239 2 C84392
373 28 58.3 240 2 G89991
374 28 58.3 255 2 D75415
375 28 58.3 257 2 A71258
376 28 58.3 262 2 E97151
377 28 58.3 265 2 JH0430
378 28 58.3 267 2 C83242
379 28 58.3 267 2 E82318
380 28 58.3 268 2 D81807
381 28 58.3 268 2 F81061
382 28 58.3 269 2 S58439
383 28 58.3 272 2 F87351
384 28 58.3 272 2 S61888
385 28 58.3 277 2 B83207
386 28 58.3 280 2 AF0649
387 28 58.3 284 2 F71467
388 28 58.3 289 2 A70604
389 28 58.3 294 2 A72362
390 28 58.3 297 2 T34165
391 28 58.3 303 2 S76535
392 28 58.3 306 2 D95273
393 28 58.3 308 2 G69135
394 28 58.3 309 2 T36244

genome polyprotein
FAB1 protein - yea
PRP8 protein homol
erythronolide synt
6-deoxyerythronoli
surfactin syntheta
dynein gamma heavi
synergomycin synth
hypothetical prote
glycine hydroxymet
glycine hydroxymet
polyketide synthas
hypothetical Bcl2/
probable exported
alpha-neurotoxin -
gp68 protein - Myc
E7 protein - human
carbon dioxide con
hypothetical prote
hypothetical prote
hypothetical prote
conserved hypotet
probable transcrip
hypothetical prote
hypothetical prote
conserved hypotet
two-component resp
hypothetical prote
hypothetical prote
hypothetical prote
probable membrane
conserved hypotet
surface antigen -
hypothetical prote
ABC transporter (A
conserved hypotet
cytochrome-C oxida
O-methyltransferas
conserved hypotet
hypothetical prote
hypothetical prote
signal sequence pe
extracellular ente
conserved hypotet
conserved hypotet
ABC transporter MD
transformation com
conserved hypotet
transcription regu
phosphomethylpyrim
phosphomethylpyrim
transcription fact
hypothetical prote
probable DNA-bindi
probable transcrip
formyltetrahydrofo
probable cell divi
hypothetical prote
cell division prot
hypothetical prote
probable phosphoe
conserved hypotet
hypothetical prote
hypothetical prote

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|--------|--------------------|-----|----|------|------|---|--------|--------------------|
| 395 | 28 | 58.3 | 323 | 2 | I49529 | transcription fact | 468 | 28 | 58.3 | 484 | 2 | AF2221 | hypothetical prote |
| 396 | 28 | 58.3 | 327 | 2 | E84137 | rhizopine ABC tran | 469 | 28 | 58.3 | 488 | 2 | S37466 | sucrose phosphoryl |
| 397 | 28 | 58.3 | 329 | 2 | T10444 | peroxidase [EC 1.1 | 470 | 28 | 58.3 | 492 | 2 | A33040 | conserved hypothet |
| 398 | 28 | 58.3 | 329 | 2 | T22221 | hypothetical prote | 471 | 28 | 58.3 | 505 | 2 | D70782 | hypothetical prote |
| 399 | 28 | 58.3 | 332 | 2 | F83600 | conserved hypothet | 472 | 28 | 58.3 | 509 | 2 | B98246 | hypothetical prote |
| 400 | 28 | 58.3 | 334 | 2 | F75344 | probable polyferre | 473 | 28 | 58.3 | 512 | 2 | T47554 | cytochrome P450 ho |
| 401 | 28 | 58.3 | 335 | 2 | JC1441 | transcription fact | 474 | 28 | 58.3 | 515 | 2 | T36714 | probable protein p |
| 402 | 28 | 58.3 | 340 | 2 | H83805 | NADH-dependent dyh | 475 | 28 | 58.3 | 517 | 2 | B70687 | hypothetical prote |
| 403 | 28 | 58.3 | 341 | 2 | S09913 | hypothetical prote | 476 | 28 | 58.3 | 533 | 2 | S76101 | hypothetical prote |
| 404 | 28 | 58.3 | 345 | 2 | B75274 | conserved hypothet | 477 | 28 | 58.3 | 538 | 2 | F69215 | adenine deaminase |
| 405 | 28 | 58.3 | 349 | 2 | T24308 | hypothetical prote | 478 | 28 | 58.3 | 544 | 2 | I55454 | neuroglycan C prec |
| 406 | 28 | 58.3 | 351 | 2 | A72844 | hypothetical prote | 479 | 28 | 58.3 | 547 | 2 | AE1022 | probable membrane |
| 407 | 28 | 58.3 | 351 | 2 | H97621 | lipopolysaccharide | 480 | 28 | 58.3 | 547 | 2 | A40656 | hypothetical prote |
| 408 | 28 | 58.3 | 353 | 2 | H84332 | carbamoyl-phosphat | 481 | 28 | 58.3 | 553 | 1 | GI8PSV | gene 1 protein - s |
| 409 | 28 | 58.3 | 353 | 2 | A95998 | probable sugar upt | 482 | 28 | 58.3 | 553 | 2 | S76949 | hypothetical prote |
| 410 | 28 | 58.3 | 358 | 2 | H69408 | carbamoyl-phosphat | 483 | 28 | 58.3 | 559 | 2 | AC3373 | NAD synthase (Gluc |
| 411 | 28 | 58.3 | 359 | 2 | B96505 | probable gibbereli | 484 | 28 | 58.3 | 566 | 2 | T31964 | hypothetical prote |
| 412 | 28 | 58.3 | 369 | 2 | A89777 | capsular polysacch | 485 | 28 | 58.3 | 570 | 2 | G85046 | hypothetical prote |
| 413 | 28 | 58.3 | 373 | 2 | H72756 | probable phosphate | 486 | 28 | 58.3 | 582 | 2 | A70755 | hypothetical prote |
| 414 | 28 | 58.3 | 374 | 2 | T21513 | hypothetical prote | 487 | 28 | 58.3 | 586 | 2 | B70503 | probable pyrG prot |
| 415 | 28 | 58.3 | 375 | 2 | AH0306 | probable exported | 488 | 28 | 58.3 | 593 | 2 | F95939 | probable adenine d |
| 416 | 28 | 58.3 | 375 | 2 | H71121 | probable alcohol d | 489 | 28 | 58.3 | 594 | 2 | AB3343 | single-stranded-DN |
| 417 | 28 | 58.3 | 377 | 2 | F71877 | alanine racemase - | 490 | 28 | 58.3 | 595 | 2 | T26843 | hypothetical prote |
| 418 | 28 | 58.3 | 382 | 2 | T28691 | hypothetical prote | 491 | 28 | 58.3 | 597 | 2 | D98186 | adenine deaminase |
| 419 | 28 | 58.3 | 384 | 2 | A72257 | probable transamin | 492 | 28 | 58.3 | 604 | 2 | AF3100 | probable centromer |
| 420 | 28 | 58.3 | 388 | 2 | D75496 | aspartate transami | 493 | 28 | 58.3 | 614 | 2 | T39740 | probable beta-gluc |
| 421 | 28 | 58.3 | 388 | 2 | S41940 | oligogalacturonide | 494 | 28 | 58.3 | 619 | 2 | T01121 | 72K mitochondrial |
| 422 | 28 | 58.3 | 388 | 2 | JQ0189 | oligogalacturonide | 495 | 28 | 58.3 | 627 | 2 | A36682 | hypothetical prote |
| 423 | 28 | 58.3 | 388 | 2 | AI0208 | oligogalacturonide | 496 | 28 | 58.3 | 631 | 2 | S46820 | hypothetical prote |
| 424 | 28 | 58.3 | 391 | 1 | TVBE11 | 44K protein kinase | 497 | 28 | 58.3 | 631 | 2 | T48255 | hypothetical prote |
| 425 | 28 | 58.3 | 392 | 2 | T48133 | hypothetical prote | 498 | 28 | 58.3 | 663 | 2 | S55164 | hypothetical prote |
| 426 | 28 | 58.3 | 395 | 2 | AB2977 | hippurate hydrolas | 499 | 28 | 58.3 | 686 | 1 | ALDYAT | amylase A (EC 3.2. |
| 427 | 28 | 58.3 | 396 | 2 | A75345 | probable chloromuc | 500 | 28 | 58.3 | 687 | 2 | S51398 | hypothetical prote |
| 428 | 28 | 58.3 | 399 | 2 | D95279 | probable alcohol f | 501 | 28 | 58.3 | 711 | 2 | A90023 | DNA topoisomerase |
| 429 | 28 | 58.3 | 399 | 2 | AE3556 | alanine racemase (| 502 | 28 | 58.3 | 712 | 1 | BVRCB | Cyab protein - Bor |
| 430 | 28 | 58.3 | 400 | 2 | T35152 | hypothetical prote | 503 | 28 | 58.3 | 731 | 1 | A55800 | cucumisin (EC 3.4. |
| 431 | 28 | 58.3 | 402 | 2 | H64599 | poly(A) polymerase | 504 | 28 | 58.3 | 739 | 1 | JQ1893 | 80.7K alpha trans- |
| 432 | 28 | 58.3 | 402 | 2 | E71912 | polynucleotide ade | 505 | 28 | 58.3 | 741 | 2 | D95966 | probable aldehyde |
| 433 | 28 | 58.3 | 404 | 2 | JC5784 | adrenomedullin rec | 506 | 28 | 58.3 | 741 | 2 | T40095 | Zinc finger, C3HC4 |
| 434 | 28 | 58.3 | 407 | 2 | S25841 | beta-ketoacyl synt | 507 | 28 | 58.3 | 742 | 1 | TNBEH1 | 80.7K alpha trans- |
| 435 | 28 | 58.3 | 408 | 2 | C95100 | aminotransferase, | 508 | 28 | 58.3 | 750 | 2 | C87159 | cation-transportin |
| 436 | 28 | 58.3 | 408 | 2 | E97968 | conserved hypothet | 509 | 28 | 58.3 | 750 | 2 | S7653 | cation-transportin |
| 437 | 28 | 58.3 | 408 | 2 | AD3237 | conserved hypothet | 510 | 28 | 58.3 | 753 | 2 | T52360 | hypothetical prote |
| 438 | 28 | 58.3 | 416 | 2 | F24723 | cryptophan synthas | 511 | 28 | 58.3 | 784 | 2 | E82731 | outer membrane ant |
| 439 | 28 | 58.3 | 416 | 2 | S76858 | hypothetical prote | 512 | 28 | 58.3 | 789 | 2 | T49065 | hypothetical prote |
| 440 | 28 | 58.3 | 419 | 2 | A85864 | hypothetical prote | 513 | 28 | 58.3 | 796 | 2 | JC7516 | vesicle protein so |
| 441 | 28 | 58.3 | 419 | 2 | G91019 | hypothetical prote | 514 | 28 | 58.3 | 820 | 2 | T32908 | hypothetical prote |
| 442 | 28 | 58.3 | 419 | 2 | S56073 | opaque-2 protein - | 515 | 28 | 58.3 | 845 | 2 | T25657 | alanine-tRNA ligas |
| 443 | 28 | 58.3 | 422 | 2 | H82236 | iron-containing al | 516 | 28 | 58.3 | 875 | 2 | A30401 | heme transport pro |
| 444 | 28 | 58.3 | 422 | 2 | A98306 | probable hydrolase | 517 | 28 | 58.3 | 877 | 2 | AC2211 | antibiotic synthet |
| 445 | 28 | 58.3 | 423 | 2 | T36467 | probable glycosyl | 518 | 28 | 58.3 | 879 | 2 | B70014 | protein-histidine |
| 446 | 28 | 58.3 | 425 | 1 | JH0710 | transcription fact | 519 | 28 | 58.3 | 904 | 2 | G64840 | sensor protein cor |
| 447 | 28 | 58.3 | 428 | 2 | I51087 | G protein-coupled | 520 | 28 | 58.3 | 904 | 2 | D90772 | sensor protein cor |
| 448 | 28 | 58.3 | 430 | 2 | D75382 | isocitrate dehydro | 521 | 28 | 58.3 | 904 | 2 | H85634 | N-methyl-D-asparta |
| 449 | 28 | 58.3 | 433 | 2 | C83271 | conserved hypothet | 522 | 28 | 58.3 | 965 | 2 | I51244 | probable ABC-type |
| 450 | 28 | 58.3 | 434 | 2 | E81139 | hypothetical prote | 523 | 28 | 58.3 | 1011 | 2 | T07712 | major tegumental a |
| 451 | 28 | 58.3 | 440 | 2 | C83368 | probable MFS trans | 524 | 28 | 58.3 | 1032 | 2 | T30270 | hypothetical prote |
| 452 | 28 | 58.3 | 445 | 2 | AD0962 | DsdX permease [imp | 525 | 28 | 58.3 | 1034 | 2 | S76134 | integrin alpha-4 c |
| 453 | 28 | 58.3 | 449 | 2 | H70526 | probable cytochrom | 526 | 28 | 58.3 | 1038 | 2 | S06046 | lysine-ketoglutar |
| 454 | 28 | 58.3 | 450 | 2 | B69198 | UDP-N-acetylmuram | 527 | 28 | 58.3 | 1056 | 2 | T02930 | protein-tyrosine k |
| 455 | 28 | 58.3 | 456 | 2 | AF0093 | Sodium sulfate sym | 528 | 28 | 58.3 | 1122 | 2 | I54237 | protein-tyrosine k |
| 456 | 28 | 58.3 | 458 | 2 | H72244 | conserved hypothet | 529 | 28 | 58.3 | 1123 | 1 | JN0712 | protein-tyrosine k |
| 457 | 28 | 58.3 | 461 | 2 | I64080 | probable membrane | 530 | 28 | 58.3 | 1124 | 1 | I58388 | protein-tyrosine k |
| 458 | 28 | 58.3 | 465 | 1 | DEBY4 | alcohol dehydrogen | 531 | 28 | 58.3 | 1125 | 1 | JH0771 | protein-tyrosine k |
| 459 | 28 | 58.3 | 465 | 2 | T70364 | dihydroliopamide d | 532 | 28 | 58.3 | 1125 | 1 | S77846 | hypothetical prote |
| 460 | 28 | 58.3 | 467 | 2 | T25848 | hypothetical prote | 533 | 28 | 58.3 | 1130 | 2 | T23104 | hypothetical prote |
| 461 | 28 | 58.3 | 467 | 2 | D85683 | ubiquinone oxidore | 534 | 28 | 58.3 | 1133 | 2 | T31066 | vascular cadherin- |
| 462 | 28 | 58.3 | 467 | 2 | H72040 | probable sodium-tr | 535 | 28 | 58.3 | 1180 | 2 | T31066 | proline ABC trans |
| 463 | 28 | 58.3 | 467 | 2 | B86225 | protein T12M4.6 li | 536 | 28 | 58.3 | 1194 | 1 | G70837 | proline ABC trans |
| 464 | 28 | 58.3 | 468 | 2 | S39832 | probable phosphopr | 537 | 28 | 58.3 | 1201 | 2 | F81202 | DNA-directed RNA p |
| 465 | 28 | 58.3 | 469 | 2 | S76891 | hypothetical prote | 538 | 28 | 58.3 | 1203 | 2 | C95229 | DNA-directed RNA p |
| 466 | 28 | 58.3 | 475 | 2 | F85430 | serine C-palmitoyl | 539 | 28 | 58.3 | 1216 | 2 | G98093 | 1-pyrroline-5-carb |
| 467 | 28 | 58.3 | 480 | 2 | G70678 | hypothetical prote | 540 | 28 | 58.3 | 1218 | 2 | AC3580 | |

| | | | | | | | | | | | | | |
|-----|------|------|------|---|--------|---------------------|-----|----|------|-----|---|--------|---------------------|
| 541 | 28 | 58.3 | 1224 | 2 | T43218 | proline dehydrogen | 614 | 27 | 56.2 | 160 | 2 | S45632 | H+-transporting tw |
| 542 | 28 | 58.3 | 1228 | 2 | C98219 | proline dehydrogen | 615 | 27 | 56.2 | 161 | 2 | T09807 | probable glutathio |
| 543 | 28 | 58.3 | 1228 | 2 | AG3067 | proline dehydrogen | 616 | 27 | 56.2 | 166 | 2 | C72641 | hypothetical prote |
| 544 | 28 | 58.3 | 1230 | 2 | H84515 | probable helicase | 617 | 27 | 56.2 | 169 | 2 | G83384 | probable ring-hydr |
| 545 | 28 | 58.3 | 1274 | 2 | E81779 | proline dehydrogen | 618 | 27 | 56.2 | 172 | 2 | T27505 | hypothetical prote |
| 546 | 28 | 58.3 | 1275 | 2 | T18556 | O-antigen biosynth | 619 | 27 | 56.2 | 174 | 2 | F83581 | heme d1 biosynthes |
| 547 | 28 | 58.3 | 1303 | 2 | C87519 | hypothetical prote | 620 | 27 | 56.2 | 183 | 2 | S53149 | core antigen - hep |
| 548 | 28 | 58.3 | 1310 | 1 | I53597 | proline dehydrogen | 621 | 27 | 56.2 | 183 | 2 | T38917 | hypothetical prote |
| 549 | 28 | 58.3 | 1320 | 1 | D64843 | proline dehydrogen | 622 | 27 | 56.2 | 190 | 2 | E84060 | hypothetical prote |
| 550 | 28 | 58.3 | 1320 | 1 | S66279 | proline dehydrogen | 623 | 27 | 56.2 | 191 | 2 | B84272 | protoporphyrinogen |
| 551 | 28 | 58.3 | 1320 | 2 | AE0633 | proline dehydrogen | 624 | 27 | 56.2 | 191 | 2 | S49826 | hypothetical prote |
| 552 | 28 | 58.3 | 1320 | 2 | D90786 | proline dehydrogen | 625 | 27 | 56.2 | 201 | 2 | B86488 | hypothetical prote |
| 553 | 28 | 58.3 | 1320 | 2 | B85646 | proline dehydrogen | 626 | 27 | 56.2 | 203 | 2 | D83236 | probable sigma-70 |
| 554 | 28 | 58.3 | 1323 | 2 | AH0225 | 1-pyrroline-5-carb | 627 | 27 | 56.2 | 206 | 2 | B69121 | hypothetical prote |
| 555 | 28 | 58.3 | 1330 | 2 | T30341 | zinc finger protei | 628 | 27 | 56.2 | 208 | 2 | T10537 | hypothetical prote |
| 556 | 28 | 58.3 | 1386 | 2 | T18434 | hypothetical prote | 629 | 27 | 56.2 | 210 | 2 | F83751 | ABC transporter (A |
| 557 | 28 | 58.3 | 1403 | 1 | A47328 | natural killer cel | 630 | 27 | 56.2 | 216 | 1 | BWPSBP | gldB protein - Pse |
| 558 | 28 | 58.3 | 1535 | 2 | S46224 | peroxidase - frui | 631 | 27 | 56.2 | 216 | 2 | I38482 | olfactory receptor |
| 559 | 28 | 58.3 | 1617 | 2 | B86483 | protein F5U5.15 [i | 632 | 27 | 56.2 | 216 | 2 | AH2547 | hypothetical prote |
| 560 | 28 | 58.3 | 1636 | 2 | B82736 | hemolysin-type cal | 633 | 27 | 56.2 | 218 | 2 | S76385 | hypothetical prote |
| 561 | 28 | 58.3 | 1640 | 2 | H88094 | protein F39E9.2 [i | 634 | 27 | 56.2 | 220 | 2 | T34986 | hypothetical prote |
| 562 | 28 | 58.3 | 1715 | 2 | G84429 | hypothetical prote | 635 | 27 | 56.2 | 224 | 1 | RGE8FT | probable secreted |
| 563 | 28 | 58.3 | 1848 | 2 | A44140 | cellulose-binding | 636 | 27 | 56.2 | 224 | 2 | AH0646 | transcription regu |
| 564 | 28 | 58.3 | 1896 | 2 | T08851 | Down syndrome cell | 637 | 27 | 56.2 | 228 | 2 | T46859 | lexA repressor pro |
| 565 | 28 | 58.3 | 1957 | 2 | T38077 | hypothetical coile | 638 | 27 | 56.2 | 229 | 2 | D86924 | cytochrome-c oxida |
| 566 | 28 | 58.3 | 2052 | 1 | S60200 | myosin X - bovine | 639 | 27 | 56.2 | 229 | 2 | D87221 | hypothetical prote |
| 567 | 28 | 58.3 | 2185 | 1 | T07084 | acetyl-CoA carboxy | 640 | 27 | 56.2 | 239 | 2 | B82123 | Hsp70 cofactor lim |
| 568 | 28 | 58.3 | 2281 | 2 | T07084 | acetyl-CoA carboxy | 641 | 27 | 56.2 | 239 | 2 | S64573 | chemotaxis protein |
| 569 | 28 | 58.3 | 2453 | 2 | S60254 | nuclear receptor c | 642 | 27 | 56.2 | 239 | 2 | A99291 | hypothetical prote |
| 570 | 28 | 58.3 | 2607 | 2 | T31678 | bacitracin synthet | 643 | 27 | 56.2 | 240 | 2 | AC2748 | hypothetical prote |
| 571 | 28 | 58.3 | 3573 | 2 | S23070 | erythronolide synt | 644 | 27 | 56.2 | 240 | 2 | B97529 | lexA repressor lim |
| 572 | 28 | 58.3 | 3643 | 2 | T36410 | probable polyketid | 645 | 27 | 56.2 | 240 | 2 | AB3357 | repressor LexA (EC |
| 573 | 28 | 58.3 | 4845 | 2 | T31067 | BIR repeat contain | 646 | 27 | 56.2 | 242 | 2 | B83738 | hypothetical prote |
| 574 | 28 | 58.3 | 5175 | 2 | T20992 | hypothetical prote | 647 | 27 | 56.2 | 242 | 2 | T48110 | hypothetical prote |
| 575 | 28 | 58.3 | 5198 | 2 | T43290 | hemikentlin precu | 648 | 27 | 56.2 | 244 | 2 | A87485 | repressor LexA lim |
| 576 | 28 | 58.3 | 6713 | 2 | B89921 | hypothetical prote | 649 | 27 | 56.2 | 245 | 2 | D70670 | hypothetical prote |
| 577 | 27.5 | 57.3 | 430 | 2 | T28143 | tapasin 1 homolog, | 650 | 27 | 56.2 | 248 | 2 | S03888 | photosystem II oxy |
| 578 | 27.5 | 57.3 | 469 | 2 | S61632 | glycine hydroxymet | 651 | 27 | 56.2 | 248 | 2 | E75302 | ABC transporter, A |
| 579 | 27 | 56.2 | 40 | 2 | S33290 | lipopolysaccharide | 652 | 27 | 56.2 | 248 | 2 | R1321 | transcription regu |
| 580 | 27 | 56.2 | 51 | 2 | T37012 | hypothetical prote | 653 | 27 | 56.2 | 249 | 2 | AF1321 | phosphate transpor |
| 581 | 27 | 56.2 | 62 | 2 | F81810 | hypothetical prote | 654 | 27 | 56.2 | 253 | 2 | E69098 | hypothetical prote |
| 582 | 27 | 56.2 | 65 | 2 | F83727 | hypothetical prote | 655 | 27 | 56.2 | 253 | 2 | T29704 | hypothetical prote |
| 583 | 27 | 56.2 | 66 | 2 | A87561 | hypothetical prote | 656 | 27 | 56.2 | 254 | 2 | T02078 | photosystem II oxy |
| 584 | 27 | 56.2 | 79 | 2 | S31013 | gene 68 protein - | 657 | 27 | 56.2 | 254 | 2 | T02873 | probable photosyst |
| 585 | 27 | 56.2 | 94 | 2 | H83655 | hypothetical prote | 658 | 27 | 56.2 | 256 | 2 | B82076 | probable general s |
| 586 | 27 | 56.2 | 99 | 2 | B97409 | hypothetical prote | 659 | 27 | 56.2 | 257 | 2 | G84712 | hypothetical prote |
| 587 | 27 | 56.2 | 104 | 2 | T23203 | hypothetical prote | 660 | 27 | 56.2 | 258 | 1 | F2TOX2 | photosystem II oxy |
| 588 | 27 | 56.2 | 107 | 2 | T23204 | hypothetical prote | 661 | 27 | 56.2 | 258 | 2 | S22763 | photosystem II oxy |
| 589 | 27 | 56.2 | 108 | 1 | CCWB | cytochrome c - ear | 662 | 27 | 56.2 | 258 | 2 | B87615 | ThiJ/PfpI family p |
| 590 | 27 | 56.2 | 112 | 1 | ASLJTX | vpu protein - huma | 663 | 27 | 56.2 | 259 | 2 | JS0771 | photosystem II oxy |
| 591 | 27 | 56.2 | 113 | 2 | F64636 | vbeB protein homol | 664 | 27 | 56.2 | 259 | 2 | D84343 | TRK potassium upta |
| 592 | 27 | 56.2 | 116 | 2 | A10746 | flagellar transcri | 665 | 27 | 56.2 | 260 | 2 | S10016 | photosystem II oxy |
| 593 | 27 | 56.2 | 119 | 1 | XMECPB | flagellar transcri | 666 | 27 | 56.2 | 260 | 2 | G82639 | hypothetical prote |
| 594 | 27 | 56.2 | 119 | 2 | B90954 | regulator of flagel | 667 | 27 | 56.2 | 261 | 2 | A90926 | hypothetical prote |
| 595 | 27 | 56.2 | 119 | 2 | F85802 | regulator of flagel | 668 | 27 | 56.2 | 261 | 2 | B85774 | hypothetical prote |
| 596 | 27 | 56.2 | 121 | 2 | S59680 | ribosomal protein | 669 | 27 | 56.2 | 261 | 2 | F64924 | probable thiosulfa |
| 597 | 27 | 56.2 | 125 | 2 | G71000 | hypothetical prote | 670 | 27 | 56.2 | 263 | 2 | JC5271 | oxygen-evolving co |
| 598 | 27 | 56.2 | 128 | 2 | G97176 | stress-induced pro | 671 | 27 | 56.2 | 263 | 2 | T02227 | NBS-LRR type resis |
| 599 | 27 | 56.2 | 129 | 2 | FC1254 | endonuclease (EC 3 | 672 | 27 | 56.2 | 263 | 2 | A83705 | phosphonates trans |
| 600 | 27 | 56.2 | 131 | 2 | AD2648 | conserved hypoteth | 673 | 27 | 56.2 | 264 | 2 | T35168 | probable transcrip |
| 601 | 27 | 56.2 | 131 | 2 | T36638 | probable substrate | 674 | 27 | 56.2 | 266 | 2 | A89775 | hypothetical prote |
| 602 | 27 | 56.2 | 133 | 2 | C97430 | hypothetical prote | 675 | 27 | 56.2 | 266 | 2 | T44344 | late competence pr |
| 603 | 27 | 56.2 | 137 | 1 | S77065 | hypothetical prote | 676 | 27 | 56.2 | 267 | 2 | C47127 | tetracenomycin C s |
| 604 | 27 | 56.2 | 138 | 2 | AD2050 | hypothetical prote | 677 | 27 | 56.2 | 271 | 2 | H90293 | hypothetical prote |
| 605 | 27 | 56.2 | 139 | 2 | D82286 | ferredoxin VC0753 | 678 | 27 | 56.2 | 272 | 2 | D84195 | oxidoeductase (im |
| 606 | 27 | 56.2 | 141 | 2 | T49659 | hypothetical prote | 679 | 27 | 56.2 | 273 | 2 | G87037 | conserved hypoteth |
| 607 | 27 | 56.2 | 142 | 2 | B70634 | probable mmpS1 pro | 680 | 27 | 56.2 | 274 | 2 | AF3291 | hypothetical prote |
| 608 | 27 | 56.2 | 144 | 2 | F27205 | hypothetical prote | 681 | 27 | 56.2 | 274 | 2 | AE3552 | high-affinity bran |
| 609 | 27 | 56.2 | 145 | 2 | T34303 | hypothetical prote | 682 | 27 | 56.2 | 282 | 2 | C71444 | probable thioester |
| 610 | 27 | 56.2 | 147 | 2 | A42435 | leech antiplatelet | 683 | 27 | 56.2 | 282 | 2 | S10773 | 2-hydroxyuconic s |
| 611 | 27 | 56.2 | 157 | 2 | D70777 | hypothetical prote | 684 | 27 | 56.2 | 283 | 2 | F95893 | probable ABC trans |
| 612 | 27 | 56.2 | 157 | 2 | F87574 | CBS domain protein | 685 | 27 | 56.2 | 284 | 2 | F81729 | signal recognition |
| 613 | 27 | 56.2 | 158 | 2 | T27757 | hypothetical prote | 686 | 27 | 56.2 | 286 | 2 | B87541 | diene lactone hydro |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|--------|--------------------|-----|----|------|-----|---|--------|---------------------|
| 687 | 27 | 56.2 | 286 | 2 | B70833 | carbon-monoxide de | 760 | 27 | 56.2 | 373 | 2 | B26470 | spore germination |
| 688 | 27 | 56.2 | 286 | 2 | B96615 | probable carbonic | 761 | 27 | 56.2 | 374 | 2 | AH0908 | probable ATP/grp-b |
| 689 | 27 | 56.2 | 287 | 2 | A81803 | probable integral | 762 | 27 | 56.2 | 375 | 2 | C75040 | alcohol dehydrogen |
| 690 | 27 | 56.2 | 288 | 2 | D81065 | hypothetical prote | 763 | 27 | 56.2 | 375 | 2 | A31142 | hypothetical prote |
| 691 | 27 | 56.2 | 291 | 2 | C97453 | cytochrome c oxida | 764 | 27 | 56.2 | 375 | 2 | B65115 | hypothetical 43.1 |
| 692 | 27 | 56.2 | 291 | 2 | AE2671 | cytochrome c oxida | 765 | 27 | 56.2 | 375 | 2 | D85987 | hypothetical prote |
| 693 | 27 | 56.2 | 291 | 2 | H75512 | formamidopyrimidin | 766 | 27 | 56.2 | 380 | 2 | B86625 | DNA-directed DNA p |
| 694 | 27 | 56.2 | 291 | 2 | A38051 | H+/K+-exchanging A | 767 | 27 | 56.2 | 380 | 2 | T30306 | DNA-directed DNA p |
| 695 | 27 | 56.2 | 294 | 2 | G72293 | phosphate butyrylt | 768 | 27 | 56.2 | 385 | 2 | G26338 | hypothetical prote |
| 696 | 27 | 56.2 | 295 | 2 | A84145 | hypothetical prote | 769 | 27 | 56.2 | 388 | 2 | F97331 | alpha/beta superfa |
| 697 | 27 | 56.2 | 300 | 1 | NDBPT7 | exodeoxyribonuclea | 770 | 27 | 56.2 | 391 | 2 | H86315 | hypothetical prote |
| 698 | 27 | 56.2 | 300 | 2 | G86829 | ribokinase (EC 2.7 | 771 | 27 | 56.2 | 391 | 2 | C94166 | hypothetical prote |
| 699 | 27 | 56.2 | 300 | 2 | AB3106 | hypothetical prote | 772 | 27 | 56.2 | 391 | 2 | T08264 | sodium-dependent p |
| 700 | 27 | 56.2 | 301 | 2 | P86749 | pseudouridine synt | 773 | 27 | 56.2 | 398 | 2 | S16275 | naringenin-chalcon |
| 701 | 27 | 56.2 | 302 | 2 | T36030 | probable fructokin | 774 | 27 | 56.2 | 398 | 2 | C84764 | membrane protein y |
| 702 | 27 | 56.2 | 302 | 2 | AG3407 | florfenicol resist | 775 | 27 | 56.2 | 400 | 2 | S70187 | 44.7K virA protein |
| 703 | 27 | 56.2 | 304 | 2 | AB2663 | 2-dehydro-3-deoxyg | 776 | 27 | 56.2 | 402 | 2 | C96781 | unknown protein F9 |
| 704 | 27 | 56.2 | 305 | 2 | T44955 | ribokinase (EC 2.7 | 777 | 27 | 56.2 | 403 | 2 | C33958 | hypothetical prote |
| 705 | 27 | 56.2 | 306 | 2 | A25698 | probable protein k | 778 | 27 | 56.2 | 405 | 2 | AF2422 | N-acyl-L-amino aci |
| 706 | 27 | 56.2 | 307 | 2 | A64449 | formylmethanofuran | 779 | 27 | 56.2 | 405 | 2 | B36807 | hypothetical prote |
| 707 | 27 | 56.2 | 307 | 2 | G75631 | probable iron-chel | 780 | 27 | 56.2 | 405 | 2 | AH2752 | dihydrolipoamide a |
| 708 | 27 | 56.2 | 308 | 1 | QQLJX1 | trans-activating t | 781 | 27 | 56.2 | 408 | 2 | PD0007 | cytochrome P450 no |
| 709 | 27 | 56.2 | 309 | 2 | B87712 | conserved hypotet | 782 | 27 | 56.2 | 408 | 2 | JC5674 | RAD23 protein homo |
| 710 | 27 | 56.2 | 311 | 2 | G86383 | probable mitochond | 783 | 27 | 56.2 | 409 | 2 | S44346 | conserved hypotet |
| 711 | 27 | 56.2 | 314 | 2 | A56650 | 2-oxoglutarate car | 784 | 27 | 56.2 | 418 | 2 | H82209 | CT011 hypothetical |
| 712 | 27 | 56.2 | 314 | 2 | A36305 | 2-oxoglutarate/mal | 785 | 27 | 56.2 | 420 | 2 | B86503 | CT011 hypothetical |
| 713 | 27 | 56.2 | 314 | 2 | H70723 | hypothetical prote | 786 | 27 | 56.2 | 420 | 2 | D72119 | CT011 hypothetical |
| 714 | 27 | 56.2 | 315 | 2 | S11081 | Na+/K+-exchanging | 787 | 27 | 56.2 | 421 | 2 | H81243 | signal recognition |
| 715 | 27 | 56.2 | 315 | 2 | B98181 | sitB protein (Arl2 | 788 | 27 | 56.2 | 421 | 2 | T44429 | probable transcrip |
| 716 | 27 | 56.2 | 316 | 2 | H95985 | probable transcrip | 789 | 27 | 56.2 | 421 | 2 | F82024 | probable signal re |
| 717 | 27 | 56.2 | 322 | 2 | H83851 | hypothetical prote | 790 | 27 | 56.2 | 422 | 2 | G90259 | hypothetical prote |
| 718 | 27 | 56.2 | 323 | 2 | T25459 | hypothetical prote | 791 | 27 | 56.2 | 422 | 2 | H90275 | hypothetical prote |
| 719 | 27 | 56.2 | 323 | 2 | A44504 | suhr protein - Rhi | 792 | 27 | 56.2 | 422 | 2 | B90327 | hypothetical prote |
| 720 | 27 | 56.2 | 323 | 2 | S19994 | acid phosphatase (| 793 | 27 | 56.2 | 424 | 2 | A30474 | hypothetical prote |
| 721 | 27 | 56.2 | 324 | 2 | B25102 | reaction center pr | 794 | 27 | 56.2 | 425 | 2 | C81551 | conserved hypotet |
| 722 | 27 | 56.2 | 325 | 2 | H81553 | hypothetical prote | 795 | 27 | 56.2 | 425 | 2 | T7241 | hypothetical prote |
| 723 | 27 | 56.2 | 325 | 2 | D86507 | hypothetical prote | 796 | 27 | 56.2 | 427 | 2 | T05019 | hypothetical prote |
| 724 | 27 | 56.2 | 325 | 2 | E72116 | hypothetical prote | 797 | 27 | 56.2 | 430 | 2 | F89923 | asparaginyl-tRNA s |
| 725 | 27 | 56.2 | 325 | 2 | T10045 | hypothetical prote | 798 | 27 | 56.2 | 430 | 2 | B95991 | asparaginyl-tRNA li |
| 726 | 27 | 56.2 | 325 | 2 | E70684 | hypothetical prote | 799 | 27 | 56.2 | 430 | 2 | H83861 | asparaginyl-tRNA s |
| 727 | 27 | 56.2 | 325 | 2 | A40963 | phospholipase A2-a | 800 | 27 | 56.2 | 430 | 2 | AH1311 | asparaginyl-tRNA s |
| 728 | 27 | 56.2 | 326 | 2 | S61517 | ficollin-1 precurs | 801 | 27 | 56.2 | 430 | 2 | AH1683 | asparaginyl-tRNA s |
| 729 | 27 | 56.2 | 329 | 2 | A97445 | hypothetical prote | 802 | 27 | 56.2 | 430 | 2 | C97160 | uracil permease ur |
| 730 | 27 | 56.2 | 333 | 2 | B86179 | hypothetical prote | 803 | 27 | 56.2 | 430 | 2 | T21060 | hypothetical prote |
| 731 | 27 | 56.2 | 340 | 2 | E69031 | conserved hypotet | 804 | 27 | 56.2 | 431 | 2 | E81053 | seryl-tRNA synthet |
| 732 | 27 | 56.2 | 341 | 2 | AH3016 | fructose biphosph | 805 | 27 | 56.2 | 435 | 2 | B82135 | menaquinone-specif |
| 733 | 27 | 56.2 | 341 | 2 | H98267 | hypothetical prote | 806 | 27 | 56.2 | 436 | 2 | B83747 | dihydrolipoamide S |
| 734 | 27 | 56.2 | 341 | 2 | A64383 | hypothetical prote | 807 | 27 | 56.2 | 436 | 2 | H69588 | acetylornithine de |
| 735 | 27 | 56.2 | 345 | 2 | E84398 | phosphate ABC tran | 808 | 27 | 56.2 | 437 | 2 | A38534 | branched-chain ami |
| 736 | 27 | 56.2 | 345 | 2 | A43586 | hypothetical prote | 809 | 27 | 56.2 | 438 | 2 | I38946 | melanoma ubiquitou |
| 737 | 27 | 56.2 | 345 | 2 | G65138 | conserved hypotet | 810 | 27 | 56.2 | 439 | 2 | H69783 | conserved hypotet |
| 738 | 27 | 56.2 | 345 | 2 | AH1514 | hypothetical prote | 811 | 27 | 56.2 | 447 | 2 | AB3359 | dihydrolipoamide S |
| 739 | 27 | 56.2 | 347 | 2 | B87500 | conserved hypotet | 812 | 27 | 56.2 | 448 | 2 | AF2198 | AAA superfamily AT |
| 740 | 27 | 56.2 | 348 | 2 | T22065 | hypothetical prote | 813 | 27 | 56.2 | 451 | 2 | T16000 | hypothetical prote |
| 741 | 27 | 56.2 | 349 | 2 | B81736 | probable 3'(2') 5' | 814 | 27 | 56.2 | 456 | 2 | G81660 | Glpt/Pept/Uhpt fam |
| 742 | 27 | 56.2 | 351 | 2 | T32717 | hypothetical prote | 815 | 27 | 56.2 | 456 | 2 | A71501 | probable hexesphos |
| 743 | 27 | 56.2 | 352 | 1 | BVECHD | molybdenum transpo | 816 | 27 | 56.2 | 457 | 2 | F97533 | dihydrolipoamide a |
| 744 | 27 | 56.2 | 352 | 2 | AE0595 | molybdenum transpo | 817 | 27 | 56.2 | 465 | 2 | AG0415 | aromatic amino aci |
| 745 | 27 | 56.2 | 352 | 2 | B85579 | ATP-binding compo | 818 | 27 | 56.2 | 470 | 2 | G87085 | arginosuccinate ly |
| 746 | 27 | 56.2 | 352 | 2 | A90728 | ATP-binding compo | 819 | 27 | 56.2 | 470 | 2 | S78440 | phosphoglucomutase |
| 747 | 27 | 56.2 | 352 | 2 | C69401 | conserved hypotet | 820 | 27 | 56.2 | 473 | 2 | A55591 | isocitrate dehydro |
| 748 | 27 | 56.2 | 354 | 2 | H82557 | hypothetical prote | 821 | 27 | 56.2 | 473 | 2 | AE2034 | isocitrate dehydro |
| 749 | 27 | 56.2 | 358 | 2 | H89954 | hypothetical prote | 822 | 27 | 56.2 | 475 | 2 | S74684 | probable prolycar |
| 750 | 27 | 56.2 | 358 | 2 | A87514 | hypothetical prote | 823 | 27 | 56.2 | 476 | 2 | G84634 | probable transport |
| 751 | 27 | 56.2 | 359 | 2 | S27788 | neutrophil oxidase | 824 | 27 | 56.2 | 476 | 2 | A83387 | hypothetical prote |
| 752 | 27 | 56.2 | 360 | 2 | C84413 | geranylgeranyl hyd | 825 | 27 | 56.2 | 478 | 2 | T32825 | hypothetical prote |
| 753 | 27 | 56.2 | 362 | 2 | A86831 | X-Pro dipeptidase | 826 | 27 | 56.2 | 488 | 2 | AD0679 | fructuronate reduc |
| 754 | 27 | 56.2 | 364 | 2 | T10945 | peroxidase (EC 1.1 | 827 | 27 | 56.2 | 490 | 2 | I48163 | signal recognition |
| 755 | 27 | 56.2 | 366 | 2 | JC4104 | orotidine-5'-phosp | 828 | 27 | 56.2 | 490 | 2 | AE2050 | NADH2 dehydrogenas |
| 756 | 27 | 56.2 | 367 | 2 | JC4103 | orotidine-5'-phosp | 829 | 27 | 56.2 | 492 | 2 | F75389 | probable aldehyde |
| 757 | 27 | 56.2 | 367 | 2 | AC2469 | hypothetical prote | 830 | 27 | 56.2 | 494 | 2 | F83206 | hypothetical prote |
| 758 | 27 | 56.2 | 372 | 2 | C81296 | carbamoyl-phosphat | 831 | 27 | 56.2 | 496 | 2 | G89824 | hypothetical prote |
| 759 | 27 | 56.2 | 373 | 2 | G69629 | germination respon | 832 | 27 | 56.2 | 507 | 2 | A39411 | glucose-6-phosphat |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|--------|---------------------|-----|----|------|------|---|--------|---------------------|
| 833 | 27 | 56.2 | 509 | 2 | E89787 | hypothetical prote | 906 | 27 | 56.2 | 802 | 2 | F70600 | hypothetical prote |
| 834 | 27 | 56.2 | 509 | 2 | JC5651 | N-acetylglucosamin | 907 | 27 | 56.2 | 813 | 2 | JC5659 | translation initia |
| 835 | 27 | 56.2 | 510 | 2 | A86143 | probable cytochrom | 908 | 27 | 56.2 | 822 | 2 | S68210 | chloride channel p |
| 836 | 27 | 56.2 | 510 | 2 | A2782 | long-chain fatty a | 909 | 27 | 56.2 | 832 | 2 | S76815 | hypothetical prote |
| 837 | 27 | 56.2 | 510 | 2 | C97561 | hypothetical prote | 910 | 27 | 56.2 | 836 | 2 | S54152 | sepB protein - Eme |
| 838 | 27 | 56.2 | 515 | 2 | G75267 | ABC transporter, p | 911 | 27 | 56.2 | 842 | 2 | T04880 | potassium transpor |
| 839 | 27 | 56.2 | 516 | 1 | S44306 | phenol 2-monooxyge | 912 | 27 | 56.2 | 859 | 2 | T35785 | probable beta-gluc |
| 840 | 27 | 56.2 | 517 | 1 | D37831 | PTS system, N-acet | 913 | 27 | 56.2 | 859 | 2 | T05470 | hypothetical prote |
| 841 | 27 | 56.2 | 523 | 2 | F82254 | adenylosuccinate l | 914 | 27 | 56.2 | 863 | 1 | SHNC | phosphoribosyl-AMP |
| 842 | 27 | 56.2 | 532 | 2 | D82666 | I2 protein - human | 915 | 27 | 56.2 | 876 | 2 | T33176 | hypothetical prote |
| 843 | 27 | 56.2 | 533 | 2 | S36594 | pyruvate dehydrog | 916 | 27 | 56.2 | 879 | 2 | T49796 | probable sepB prot |
| 844 | 27 | 56.2 | 538 | 2 | A48692 | probable membrane | 917 | 27 | 56.2 | 880 | 2 | AC2108 | alanine-CRNA synthe |
| 845 | 27 | 56.2 | 545 | 2 | AB0290 | 60K cysteine-rich | 918 | 27 | 56.2 | 885 | 1 | S26723 | DNA-directed RNA p |
| 846 | 27 | 56.2 | 547 | 1 | A32244 | 60K cysteine-rich | 919 | 27 | 56.2 | 887 | 2 | AS4832 | villin homolog qua |
| 847 | 27 | 56.2 | 547 | 2 | B43584 | alpha, alpha-phosph | 920 | 27 | 56.2 | 891 | 2 | AC0149 | DNA topoisomerase |
| 848 | 27 | 56.2 | 548 | 2 | AF1231 | alpha, alpha-phosph | 921 | 27 | 56.2 | 901 | 2 | H64101 | preprotein translo |
| 849 | 27 | 56.2 | 548 | 2 | AE1585 | chaperonin - Metha | 922 | 27 | 56.2 | 907 | 2 | S23399 | chloride channel p |
| 850 | 27 | 56.2 | 552 | 2 | H69126 | 60K cysteine-rich | 923 | 27 | 56.2 | 917 | 2 | S51254 | STE5 protein - yea |
| 851 | 27 | 56.2 | 553 | 2 | D71515 | hypothetical prote | 924 | 27 | 56.2 | 918 | 2 | S04255 | regulatory protein |
| 852 | 27 | 56.2 | 556 | 2 | S75873 | urocanate hydratase | 925 | 27 | 56.2 | 919 | 2 | C87445 | DNA gyrase subunit |
| 853 | 27 | 56.2 | 558 | 2 | B75611 | phosphorylase kina | 926 | 27 | 56.2 | 920 | 2 | C70668 | probable mmpL7 pro |
| 854 | 27 | 56.2 | 560 | 2 | S51600 | hypothetical prote | 927 | 27 | 56.2 | 966 | 2 | S18955 | fix23-3 protein - |
| 855 | 27 | 56.2 | 562 | 2 | H70888 | integral membrane | 928 | 27 | 56.2 | 987 | 2 | A75496 | conserved hypothet |
| 856 | 27 | 56.2 | 564 | 2 | S75777 | alkaline phosphata | 929 | 27 | 56.2 | 987 | 2 | I48373 | G-utrophin - mouse |
| 857 | 27 | 56.2 | 564 | 2 | F87305 | probable membrane | 930 | 27 | 56.2 | 1002 | 2 | T30546 | major surface glyc |
| 858 | 27 | 56.2 | 567 | 2 | AC0754 | DNA repair protein | 931 | 27 | 56.2 | 1046 | 2 | S67786 | hypothetical prote |
| 859 | 27 | 56.2 | 568 | 2 | B87495 | acetolactate synth | 932 | 27 | 56.2 | 1059 | 1 | A35210 | ferroxidase (EC 1. |
| 860 | 27 | 56.2 | 571 | 2 | F84956 | hypothetical prote | 933 | 27 | 56.2 | 1062 | 2 | S61196 | SUM1 protein - yea |
| 861 | 27 | 56.2 | 571 | 2 | G84426 | pyruvate dehydrog | 934 | 27 | 56.2 | 1063 | 2 | T00624 | endo-1,4-beta-xyla |
| 862 | 27 | 56.2 | 572 | 2 | AG0608 | probable oxidoredu | 935 | 27 | 56.2 | 1076 | 2 | B85295 | probable DNA misem |
| 863 | 27 | 56.2 | 574 | 2 | C83359 | hypothetical prote | 936 | 27 | 56.2 | 1076 | 2 | T05793 | mah3 protein homol |
| 864 | 27 | 56.2 | 577 | 2 | E71364 | hypothetical prote | 937 | 27 | 56.2 | 1078 | 2 | PC4198 | peptide synthetase |
| 865 | 27 | 56.2 | 578 | 2 | T19023 | hypothetical prote | 938 | 27 | 56.2 | 1081 | 2 | T51613 | DNA mismatch repai |
| 866 | 27 | 56.2 | 582 | 2 | F82064 | conserved hypothet | 939 | 27 | 56.2 | 1121 | 2 | T47970 | hypothetical prote |
| 867 | 27 | 56.2 | 588 | 2 | B87521 | peptidase M1 famil | 940 | 27 | 56.2 | 1148 | 2 | F69685 | pyruvate carboxyla |
| 868 | 27 | 56.2 | 590 | 1 | A54372 | G protein-coupled | 941 | 27 | 56.2 | 1159 | 2 | T13946 | probable adaptor-r |
| 869 | 27 | 56.2 | 596 | 2 | G69038 | dnak-type molecula | 942 | 27 | 56.2 | 1225 | 2 | B95229 | DNA-directed RNA p |
| 870 | 27 | 56.2 | 598 | 2 | T48822 | hypothetical prote | 943 | 27 | 56.2 | 1225 | 2 | F98093 | DNA-binding protei |
| 871 | 27 | 56.2 | 599 | 2 | S18735 | centromere protein | 944 | 27 | 56.2 | 1235 | 1 | Q0BEW4 | structural polypro |
| 872 | 27 | 56.2 | 602 | 2 | T21980 | hypothetical prote | 945 | 27 | 56.2 | 1254 | 1 | JQ1978 | hypothetical prote |
| 873 | 27 | 56.2 | 607 | 2 | S96598 | DNA polymerase III | 946 | 27 | 56.2 | 1254 | 2 | T47141 | hypothetical prote |
| 874 | 27 | 56.2 | 608 | 2 | B87282 | hypothetical prote | 947 | 27 | 56.2 | 1289 | 2 | S69689 | hypothetical prote |
| 875 | 27 | 56.2 | 610 | 2 | G72494 | ABC transporter, A | 948 | 27 | 56.2 | 1291 | 2 | T17242 | hypothetical prote |
| 876 | 27 | 56.2 | 619 | 2 | G75321 | carbon-monoxide de | 949 | 27 | 56.2 | 1302 | 2 | B41349 | multidrug resistan |
| 877 | 27 | 56.2 | 622 | 1 | H69480 | phosphorotene pho | 950 | 27 | 56.2 | 1329 | 2 | A64828 | cell division prot |
| 878 | 27 | 56.2 | 623 | 2 | S68963 | ABC transporter AT | 951 | 27 | 56.2 | 1330 | 1 | GQFFE | epidermal growth f |
| 879 | 27 | 56.2 | 626 | 2 | A13310 | hypothetical prote | 952 | 27 | 56.2 | 1342 | 2 | B85614 | cell division prot |
| 880 | 27 | 56.2 | 628 | 2 | T20714 | conserved hypothet | 953 | 27 | 56.2 | 1342 | 2 | G90750 | cell division prot |
| 881 | 27 | 56.2 | 628 | 2 | H89917 | probable polygalac | 954 | 27 | 56.2 | 1343 | 2 | AF0611 | hypothetical prote |
| 882 | 27 | 56.2 | 629 | 2 | T07426 | hypothetical prote | 955 | 27 | 56.2 | 1374 | 2 | D72593 | hypothetical prote |
| 883 | 27 | 56.2 | 629 | 2 | T25571 | ribosomal protein | 956 | 27 | 56.2 | 1385 | 2 | T25828 | hypothetical prote |
| 884 | 27 | 56.2 | 633 | 2 | C32571 | outer membrane pro | 957 | 27 | 56.2 | 1441 | 2 | B86807 | nuclear pore compl |
| 885 | 27 | 56.2 | 634 | 2 | A64521 | hypothetical prote | 958 | 27 | 56.2 | 1475 | 2 | S42718 | hypothetical prote |
| 886 | 27 | 56.2 | 638 | 2 | T48380 | O-succinylhomoseri | 959 | 27 | 56.2 | 1533 | 2 | F71274 | ClaHrin heavy cha |
| 887 | 27 | 56.2 | 639 | 2 | S57153 | probable penicilli | 960 | 27 | 56.2 | 1681 | 2 | S42369 | serine/threonine k |
| 888 | 27 | 56.2 | 652 | 2 | C71285 | probable outer mem | 961 | 27 | 56.2 | 1799 | 2 | AD1895 | acetyl-CoA carboxy |
| 889 | 27 | 56.2 | 668 | 2 | A71986 | harpin secretion | 962 | 27 | 56.2 | 1822 | 2 | T02035 | probable protein t |
| 890 | 27 | 56.2 | 697 | 2 | A49313 | conserved hypothet | 963 | 27 | 56.2 | 2325 | 2 | T02035 | hypothetical prote |
| 891 | 27 | 56.2 | 705 | 2 | S55420 | chemotaxis protein | 964 | 27 | 56.2 | 2374 | 2 | T21052 | hypothetical prote |
| 892 | 27 | 56.2 | 720 | 2 | C82380 | hypothetical prote | 965 | 27 | 56.2 | 2783 | 2 | T31431 | inositol 1,4,5-tri |
| 893 | 27 | 56.2 | 720 | 2 | S75935 | hypothetical prote | 966 | 27 | 56.2 | 3187 | 2 | JCS837 | 364K Golgi complex |
| 894 | 27 | 56.2 | 724 | 1 | B32571 | ribosomal protein | 967 | 27 | 56.2 | 3433 | 1 | S28381 | utrophin - human |
| 895 | 27 | 56.2 | 726 | 2 | D72409 | pyrophosphatase, p | 968 | 27 | 56.2 | 3972 | 2 | S75251 | hypothetical prote |
| 896 | 27 | 56.2 | 733 | 2 | F84476 | probable Athila re | 969 | 27 | 56.2 | 4859 | 2 | S74173 | ryanodine receptor |
| 897 | 27 | 56.2 | 735 | 2 | I51901 | ribosomal protein | 970 | 27 | 56.2 | 4861 | 2 | S71752 | giant protein p619 |
| 898 | 27 | 56.2 | 735 | 2 | A53300 | ribosomal protein | 971 | 27 | 56.2 | 4868 | 2 | B54161 | ryanodine-binding |
| 899 | 27 | 56.2 | 740 | 2 | I38556 | ribosomal protein | 972 | 27 | 56.2 | 4869 | 2 | S66572 | ryanodine receptor |
| 900 | 27 | 56.2 | 752 | 1 | A32571 | ATP-dependent RNA | 973 | 27 | 56.2 | 4872 | 2 | S27272 | ryanodine receptor |
| 901 | 27 | 56.2 | 759 | 2 | G69258 | RNA mismatch repai | 974 | 27 | 56.2 | 4967 | 2 | S72269 | ryanodine receptor |
| 902 | 27 | 56.2 | 776 | 2 | E86830 | hypothetical prote | 975 | 27 | 56.2 | 4969 | 2 | A37113 | ryanodine receptor |
| 903 | 27 | 56.2 | 776 | 2 | T19900 | secreted protease | 976 | 27 | 56.2 | 5032 | 1 | A35041 | ryanodine receptor |
| 904 | 27 | 56.2 | 781 | 2 | G96991 | protein H14A12.6 [| 977 | 27 | 56.2 | 5035 | 1 | I46646 | ryanodine-binding |
| 905 | 27 | 56.2 | 794 | 2 | F88508 | | 978 | 27 | 56.2 | 5037 | 1 | A54161 | |

```

979 27 56.2 5037 2 B35041 ryanodine receptor
980 27 56.2 7463 2 T32248 CDA peptide synthe
981 27 56.2 13055 2 T16580 hypothetical prote
982 26.5 55.2 132 2 E86917 conserved hypothet
983 26.5 55.2 132 2 F70654 hypothetical prote
984 26.5 55.2 173 2 A72625 hypothetical prote
985 26.5 55.2 332 2 D95973 probable sugar upt
986 26.5 55.2 395 2 S78793 hypothetical prote
987 26.5 55.2 439 2 B82114 flagellum-specific
988 26.5 55.2 1186 2 S72229 meiotic recombinat
989 26.5 55.2 1205 2 T18517 procollagen N-endo
990 26.5 55.2 1292 2 T09229 galactose binding
991 26 54.2 36 2 A69827 hypothetical prote
992 26 54.2 56 2 A49619 cellular adhesion
993 26 54.2 64 2 D97979 hypothetical prote
994 26 54.2 64 2 G85659 hypothetical prote
995 26 54.2 77 2 B82441 hypothetical prote
996 26 54.2 77 2 D89887 hypothetical prote
997 26 54.2 84 2 S63410 hypothetical prote
998 26 54.2 84 2 S63323 hypothetical prote
999 26 54.2 84 2 D70967 hypothetical prote
1000 26 54.2 92 2 C27733 hypothetical prote

ALIGNMENTS

RESULT 1
S24712
Ig alpha chain - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 05-Nov-1999
C:Accession: S24712
R:Tsapis, A.
submitted to the EMBL Data Library, August 1992
A:Reference number: S24708
A:Accession: S24712
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-83 <TSA>
A:Cross-references: EMBL:Z14963; NID:G28571; PIDN:CAA78686.1; PID:G28572
C:Keywords: immunoglobulin

Query Match 79.2%; Score 38; DB 2; Length 83;
Best Local Similarity 77.8%; Pred. No. 0.93;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPHETITAL 9
DB 22 GPHETTTP 30

RESULT 2
T35421
probable regulatory protein - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C:Accession: T35421
R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, March 1999
A:Reference number: Z21577
A:Accession: T35421
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-404 <OLI>
A:Cross-references: UNIPROT:Q9X7X6; EMBL:AL049485; PIDN:CAB39714.1; GSPDB:GN00070; SCOE
A:Experimental source: strain A3 (2)
C:Genetics:
A:Gene: SCORDB:SC6A5.30C

Query Match 77.1%; Score 37; DB 2; Length 404;
Best Local Similarity 66.7%; Pred. No. 8.9;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

QY 1 GPHETITAL 9
DB 296 GPEHVAAL 304

RESULT 3

E86726
cell division protein FtsY [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
A:Accession: E86726
R:Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssi
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: E86726
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-459 <STO>
A:Cross-references: UNIPROT:Q9CHB9; GB:AE005176; PID:G12723735; PIDN:AAK04911.1; GSPDB:G
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: ftsY
C:Superfamily: cell division protein ftsY

Query Match 75.0%; Score 36; DB 2; Length 459;
Best Local Similarity 87.5%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PHETITAL 9
DB 374 PHETITAL 381

RESULT 4

C88400
protein H19M22.1 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
A:Accession: C88400
R:Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A:Reference number: A75000; MUID:99069613; PMID:9851916
A>Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/Projects/C_eleg
A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: C88400
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1825 <STO>
A:Cross-references: UNIPROT:Q9UB28; UNIPROT:Q9UB29; GB:chr_III; PIDN:AAB94997.1; PID:G974
C:Genetics:
A:Gene: H19M22.1
A:Map position: 3

Query Match 75.0%; Score 36; DB 2; Length 1825;
Best Local Similarity 77.8%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPHETITAL 9
DB 288 GPHFTITGL 296

RESULT 5

T32828
hypothetical protein H19M22.1 - Caenorhabditis elegans (fragment)
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
A:Accession: T32828
R:Wilson, R.; Wamsley, P.
submitted to the EMBL Data Library, December 1997

A;Description: The sequence of C. elegans cosmid H19M22.

A;Reference number: Z21229

A;Accession: T32828

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1825 <MIL>

A;Cross-references: UNIPROT:Q9UB28; UNIPROT:Q9UB29; EMBL:AF040648; PIDN:AAB94997.1; GSPD

A;Experimental source: strain Bristol N2; clone H19M22

C;Genetics:

A;Gene: C8SP.H19M22.1

A;Map position: 3

A;Introns: 271/2

Query Match 75.0%; Score 36; DB 2; Length 1825;

Best Local Similarity 77.8%; Pred. No. 78;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPHETITL 9

|||||

288 GPHFTITGL 296

RESULT 6

A12205

hypothetical protein alr3200 [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C;Accession: A12205

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: A12205

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-201 <KUR>

A;Cross-references: UNIPROT:Q8YS91; GB:BA000019; PIDN:BA074899.1; PID:g17132295; GSPDB:C

A;Experimental source: strain PCC 7120

C;Genetics:

A;Gene: alr3200

Query Match 72.9%; Score 35; DB 2; Length 201;

Best Local Similarity 71.4%; Pred. No. 11;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPHETIT 7

|||||

38 GPHETVS 44

RESULT 7

AB0936

N-acetyl-gamma-glutamyl-phosphate reductase [imported] - Salmonella enterica subsp. ente

C;Species: Salmonella enterica subsp. enterica serovar Typhi

A;Note: this species has also been called Salmonella typhi

C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002

C;Accession: AB0936

R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,

th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,

S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AB0936

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-334 <PAR>

A;Cross-references: GB:AL513382; PIDN:CAD09508.1; PID:g16504625; GSPDB:GN00176

C;Genetics:

A;Gene: STV3752

C;Superfamily: N-acetyl-gamma-glutamyl-phosphate reductase

Query Match 72.9%; Score 35; DB 2; Length 334;

Best Local Similarity 87.5%; Pred. No. 19;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 PHETITL 9

|||||

25 PHMTITL 32

RESULT 8

T06595

2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase (EC 2.7.6.3) - garden f

N;Contains: 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase (EC 2.7

C;Species: Pisum sativum (garden pea)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: T06595

R;Rebelle, F.; Machereel, D.; Mouillon, J.M.; Garin, J.; Douce, R.

EMBO J. 16, 947-957, 1997

A;Title: Folate biosynthesis in higher plants: purification and molecular cloning of a b

ochondria.

A;Reference number: Z15785; MUID:97224122; PMID:9118956

A;Accession: T06595

A;Status: translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-515 <REB>

A;Cross-references: UNIPROT:O04862; EMBL:Y08611; NID:g1934971; PIDN:CAA69903.1; PID:g1934

A;Note: parts of this sequence, including the amino end of the mature protein, were dete

C;Function: <HPPK>

A;Description: EC 2.7.6.3 [validated, MUID:97224122]

A;Pathway: folate biosynthesis

C;Function: <DHFS>

A;Description: EC 2.5.1.15 [validated, MUID:97224122]

A;Pathway: folate biosynthesis

A;Note: cofactor Mg(2+)

C;Superfamily: bifunctional folic acid synthesis protein; 2-amino-4-hydroxy-6-hydroxymet

C;Keywords: diphosphotransferase; folate biosynthesis; mitochondrion

F;1-28/Domain: transit peptide (mitochondrion) #status predicted <TNP>

F;29-515/Product: bifunctional folic acid synthesis protein #status experimental <MAT>

F;48-179/Domain: 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase hom

F;232-488/Domain: dihydropterate synthase homology <DHS>

Query Match 72.9%; Score 35; DB 1; Length 515;

Best Local Similarity 66.7%; Pred. No. 31;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPHETITL 9

|||||

107 GPHELLAAL 115

RESULT 9

B71404

hypothetical protein - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

A;Variety: Columbia

C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 09-Jul-2004

C;Accession: B71404

R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk

P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenecker, T.; Pohl, T.M.; Terry, N.; Giel

avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.

Nature 391, 485-488, 1998

A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech

erhoft, A.; Moore, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans

C.; Chalwatzi, N.

A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal

A;Reference number: A71400; MUID:98121113; PMID:9461215

A;Accession: B71404

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-724 <BBV>

A;Cross-references: UNIPROT:O23283; GB:Z97335; NID:g2244747; PID:e326878; PID:g2244781

C:Genetics:
A:Map position: 4COP9-4G3B45

Query Match 72.9%; Score 35; DB 2; Length 724;
Best Local Similarity 66.7%; Pred. No. 45;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPHETITAL 9
|||||:|
Db 526 GPHENIASL 534

RESULT 10
VHWVEV
structural polyprotein - eastern equine encephalomyelitis virus (strain 82V-2137)
N:Contains: 6K protein; coat protein C; membrane glycoprotein E1; membrane glycoprotein
C:Species: eastern equine encephalomyelitis virus
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C:Accession: A26816
R:Chang, G.J.J.; Trent, D.W.
J. Gen. Virol. 68, 2129-2142, 1987
A:Title: Nucleotide sequence of the genome region encoding the 26S mRNA of eastern equine
A:Reference number: A26816; MUID:87282265; PMID:2886548
A:Accession: A26816
A:Molecule type: mRNA
A:Residues: 1-1239 <CHA>
A:Cross-references: UNIPROT:P08768; EMBL:X05816; NID:G62074; PIDN:CAA29261.1; PID:G62075
C:Superfamily: togavirus structural polyprotein
C:Keywords: coat protein; glycoprotein; transmembrane protein
F:1-259/Product: coat protein C #status predicted <CPC>
F:260-322/Product: membrane glycoprotein E3 #status predicted <MG3>
F:261-277/Domain: transmembrane #status predicted <TN1>
F:323-743/Product: membrane glycoprotein E2 #status predicted <MG2>
F:684-701/Domain: transmembrane #status predicted <TN2>
F:727-737/Domain: transmembrane #status predicted <TN3>
F:743-798/Domain: transmembrane #status predicted <K6P>
F:777-798/Domain: transmembrane #status predicted <TN4>
F:799-1239/Product: membrane glycoprotein E1 #status predicted <MG1>
F:1211-1235/Domain: transmembrane #status predicted <TN5>
F:49,270,624,637,932/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 72.9%; Score 35; DB 1; Length 1239;
Best Local Similarity 75.0%; Pred. No. 82;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PHETITAL 9
|||||:|
Db 289 PHETLTM 296

RESULT 11
VHWVEV
structural polyprotein - eastern equine encephalomyelitis virus (strain VA33[Ten Broeck])
N:Contains: 6K protein; coat protein C; membrane glycoprotein E1; membrane glycoprotein
C:Species: eastern equine encephalomyelitis virus
A:Note: host Equus caballus (domestic horse)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: A39992
R:Weaver, S.C.; Scott, T.W.; Rico-Hesse, R.
Virology 182, 774-784, 1991
A:Title: Molecular evolution of eastern equine encephalomyelitis virus in North America.
A:Reference number: A39992; MUID:91220727; PMID:2024496
A:Accession: A39992
A:Molecule type: Genomic RNA
A:Residues: 1-1240 <WEA>
A:Cross-references: UNIPROT:P27284; GB:M69094; NID:G323696; PIDN:AAA42980.1; PID:G323697
A:Note: the authors translated the codon AGC for residue 836 as Arg and GUU for residue
C:Superfamily: togavirus structural polyprotein
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F:1-260/Product: coat protein C #status predicted <CPC>
F:259-276/Domain: transmembrane #status predicted <TN1>
F:261-323/Product: membrane glycoprotein E3 #status predicted <EG3>
F:324-743/Product: membrane glycoprotein E2 #status predicted <EG2>

F:695-712/Domain: transmembrane #status predicted <TM2>
F:722-738/Domain: transmembrane #status predicted <TM3>
F:744-799/Product: 6K protein #status predicted <KP6>
F:781-799/Domain: transmembrane #status predicted <TM4>
F:800-1240/Product: membrane glycoprotein E1 #status predicted <EG1>
F:1212-1236/Domain: transmembrane #status predicted <TM5>
F:49,271,625,638,834,933/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 72.9%; Score 35; DB 1; Length 1240;
Best Local Similarity 75.0%; Pred. No. 82;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PHETITAL 9
|||||:|
Db 290 PHETLTM 297

RESULT 12
S26373
genome polyprotein - eastern equine encephalomyelitis virus
N:Contains: 6K protein; capsid protein C; envelope protein E1; envelope protein E2; envelope
C:Species: eastern equine encephalomyelitis virus
C:Date: 06-Jan-1994 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C:Accession: S26373
R:Volchikov, V.E.; Volchkova, V.A.; Netesov, S.V.
Mol. Gen. Mikrobiol. Virusol. 5, 8-15, 1991
A:Title: Complete nucleotide sequence of the eastern equine encephalomyelitis virus genom
A:Reference number: S26369; MUID:91375524; PMID:1896061
A:Accession: S26373
A:Molecule type: mRNA
A:Residues: 1-1241 <VOL>
A:Cross-references: UNIPROT:O66579; EMBL:X63135; NID:G59185; PIDN:CAA44845.1; PID:G59186
A:Note: sequence could not be checked because of bad print in paper
C:Superfamily: togavirus structural polyprotein
C:Keywords: capsid protein; envelope protein; glycoprotein; polyprotein
F:1-260/Product: capsid protein C #status predicted <CAP>
F:261-323/Product: envelope protein E3 #status predicted <EP3>
F:324-743/Product: envelope protein E2 #status predicted <EP2>
F:744-800/Product: 6K protein #status predicted <K6P>
F:801-1241/Product: envelope protein E1 #status predicted <EP1>

Query Match 72.9%; Score 35; DB 2; Length 1241;
Best Local Similarity 75.0%; Pred. No. 82;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PHETITAL 9
|||||:|
Db 290 PHETLTM 297

RESULT 13
A56605
structural polyprotein - eastern equine encephalomyelitis virus (strain 4789)
C:Species: eastern equine encephalomyelitis virus
C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004
C:Accession: A56605
R:Weaver, S.C.; Hagenbaugh, A.; Bellew, L.A.; Calisher, C.H.
Arch. Virol. 127, 305-314, 1992
A:Title: Genetic characterization of an antigenic subtype of eastern equine encephalomyel
A:Reference number: A56605; MUID:93090093; PMID:1280945
A:Accession: A56605
A>Status: preliminary
A:Molecule type: Genomic RNA
A:Residues: 1-1242 <WEA>
A:Cross-references: UNIPROT:Q08359; GB:L20951; NID:G405814; PIDN:AAA02897.1; PID:G305047
A:Note: sequence inconsistent with nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBI:119924, NCBI:P:119931)
C:Superfamily: togavirus structural polyprotein
C:Keywords: polyprotein

Query Match 72.9%; Score 35; DB 2; Length 1242;
Best Local Similarity 75.0%; Pred. No. 82;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PHETITAL 9
 Db 291 PHETLTM 298
 RESULT 14
 S72350
 structural polyprotein - eastern equine encephalomyelitis virus
 N:Contains: GK protein; capsid protein; E1 protein; E2 protein; E3 protein
 C:Species: eastern equine encephalomyelitis virus
 C>Date: 04-May-1998 #sequence_revision 15-May-1998 #text_change 09-Jul-2004
 C:Accession: S72350
 R:Weaver, S.C.; Hagenbaugh, A.; Bellow, L.A.; Neteosov, S.V.; Volchikov, V.E.; Chang, G.J.
 Virolgy 197, 375-390, 1993
 A:Title: A comparison of the nucleotide sequences of eastern and western equine encephalomyelitis virus
 A:Reference number: S72349; MUID:94025587; PMID:8105605
 A:Accession: S72350
 A:Status: preliminary
 A:Molecule type: genomic RNA
 A:Residues: 1-1242 <WEA>
 A:Cross-references: UNIPROT:Q88790; EMBL:U01034; NID:g393006; PIDN:AAC53735.1; PID:g393006
 C:Superfamily: togavirus structural polyprotein
 Query Match 72.9%; Score 35; DB 2; Length 1242;
 Best Local Similarity 75.0%; Pred. No. 82;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 PHETITAL 9
 Db 291 PHETLTM 298
 RESULT 15
 T14070
 peptide synthetase - Streptomyces fradiae (fragment)
 C:Species: Streptomyces fradiae
 C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C:Accession: T14070
 R:Hosted, T.J.; Baltz, R.H.
 submitted to the EMBL Data Library, July 1997
 A:Reference number: Z17868
 A:Accession: T14070
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1324 <HOS>
 A:Cross-references: UNIPROT:O52048; EMBL:AF016696; NID:g2738764; PID:g2738765; PIDN:AAC60700
 C:Genetics:
 C:Note: cpe-1
 C:Superfamily: Mycobacterium tuberculosis mbe protein; acetate-CoA ligase homology; acyl carrier protein; phosphopantetheine; phosphoprotein
 F:188-642/Domain: acetate-CoA ligase homology <ACL>
 F:659-727/Domain: acyl carrier protein homology <ACP>
 F:691/Binding site: phosphopantetheine (Ser) (covalent) #status predicted
 Query Match 72.9%; Score 35; DB 2; Length 1324;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GPHEITI 6
 Db 659 GPHEITI 664
 RESULT 16
 A70573
 hypothetical protein Rv2626c - Mycobacterium tuberculosis (strain H37RV)
 C:Species: Mycobacterium tuberculosis
 C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
 C:Accession: A70573
 R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Cole, S.T.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Connor, R.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 406, 959-964, 2000

Nature 393, 537-544, 1998
 A:Authors: Soares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987; PMID:9634230
 A:Accession: A70573
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-143 <COL>
 A:Cross-references: UNIPROT:O06186; GB:Z95387; GB:AL123456; NID:g3261763; PIDN:CAB08616.1
 A:Experimental source: strain H37RV
 C:Genetics:
 A:Gene: Rv2626c
 C:Superfamily: conserved hypothetical protein yhcV; CBS homology
 F:77-124/Domain: CBS homology <CBS>
 Query Match 70.8%; Score 34; DB 2; Length 143;
 Best Local Similarity 75.0%; Pred. No. 12;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GPHEITI 8
 Db 16 GEHETLTA 23
 RESULT 17
 T40860
 probable alpha-amylase precursor SPC11E10.09c - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: T40860; T41181
 R:Ramsperger, U.; Pohl, T.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, October 1999
 A:Reference number: Z21952
 A:Accession: T40860
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-478 <RAM>
 A:Cross-references: UNIPROT:Q10427; EMBL:AL121783; NID:g6016988; PIDN:CAB57851.1; PID:g6016988
 A:Experimental source: strain 972h-; cosmid c11E10
 R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Seeger, K.; Harris, D.
 submitted to the EMBL Data Library, April 1999
 A:Reference number: Z21976
 A:Accession: T41181
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-203 <LYN>
 A:Cross-references: EMBL:AL049662; NID:g4678680; PIDN:CABA1221.1; PID:g4678681; GSPDB:GN000000000
 A:Experimental source: strain 972h-; cosmid c188
 C:Genetics:
 A:Gene: SPDB:SPC11E10.09c; SPDB:SPC1188.01c
 A:Map position: 3
 A:Introns: 320/3; 468/3
 C:Superfamily: Aspergillus alpha-amylase; alpha-amylase core homology
 Query Match 70.8%; Score 34; DB 2; Length 478;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 PHETIT 7
 Db 168 PHETIT 173
 RESULT 18
 G82971
 Probable ferredoxin PA5399 [imported] - Pseudomonas aeruginosa (strain PA01)
 C:Species: Pseudomonas aeruginosa
 C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C:Accession: G82971
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; Lim, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, ; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000

A:Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: G82971
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-653 <STO>
A:Cross-references: UNIPROT:Q9HTG5; GB:AS004952; GB:AS004091; NID:G9951718; PIDN:AAG0878
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA5399

Query Match 70.8%; Score 34; DB 2; Length 653;
Best Local Similarity 66.7%; Pred. No. 65;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPHETITALL 9
|||:||||
Db 301 GPHQPIVAL 309

RESULT 19
D87196
probable membrane protein [imported] - *Mycobacterium leprae*
C:Species: *Mycobacterium leprae*
C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: D87196
R:Coile, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Hildebrand, R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd, S.; Rutter, J.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Taylor, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Squares, S.; Taylor, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Massive gene decay in the leprosy bacillus.
A:Cross-references: UNIPROT:Q9CB97; GB:AL450380; NID:gl3093921; PIDN:CAC31812.1; GSPDB:G31812.1
A:Reference number: A86909; MUID:21128732; PMID:11234002
A:Accession: D87196
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-181 <STO>
A:Cross-references: UNIPROT:Q9CB97; GB:AL450380; NID:gl3093921; PIDN:CAC31812.1; GSPDB:G31812.1
C:Genetics:
A:Gene: ML2296
C:Superfamily: *Mycobacterium tuberculosis* hypothetical protein Rv3669

Query Match 68.8%; Score 33; DB 2; Length 181;
Best Local Similarity 55.6%; Pred. No. 25;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GPHETITALL 9
|||:||||
Db 130 GPHQTIESV 138

RESULT 20
C70530
hypothetical protein Rv2696c - *Mycobacterium tuberculosis* (strain H37Rv)
C:Species: *Mycobacterium tuberculosis*
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: C70530
R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Taylor, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Authors: Squares, R.; Suleston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: C70530
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-259 <COL>
A:Cross-references: UNIPROT:O07198; GB:Z96072; GB:AL123456; NID:G3261793; PIDN:CAB09486
A:Experimental source: strain H37Rv
C:Genetics:
A:Gene: Rv2696c

| | | | | | | | | | | | | | | |
|---|--|--|----------|------------|---------|--------|--------------|------|------------|----|--------|----|------|----|
| | Best Local Similarity | 62.5%; | Pred.No. | 88; | Matches | 5; | Conservative | 2; | Mismatches | 1; | Indels | 0; | Gaps | 0; |
| Qy | 2 PHEITITAL 9 : DB | 347 PHQNVTAL 354 | | | | | | | | | | | | |
| RESULT 25 | | | | | | | | | | | | | | |
| S56342 | YidB protein - Escherichia coli (strain K-12) | | | | | | | | | | | | | |
| C: | Species: Escherichia coli | | | | | | | | | | | | | |
| C: | Date: | 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004 | | | | | | | | | | | | |
| C: | Accession: | S56342; A65221 | | | | | | | | | | | | |
| R: | Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R. | | | | | | | | | | | | | |
| Nucleic Acids Res. | 23, | 2105-2119, 1995 | | | | | | | | | | | | |
| A: | Title: | Analysis of the Escherichia coli genome VI: DNA sequence of the region | | | | | | | | | | | | |
| A: | Reference number: | S56314; MUID:95334362; PMID:7610040 | | | | | | | | | | | | |
| A: | Accession: | S56342 | | | | | | | | | | | | |
| A: | Status: | preliminary; nucleic acid sequence not shown; translation not shown | | | | | | | | | | | | |
| A: | Molecule type: | DNA | | | | | | | | | | | | |
| A: | Residues: | 1-557 <BUR> | | | | | | | | | | | | |
| A: | Cross-references: | UNIPROT:Q8XEJ3; EMBL:U14003; NID:g1263172; PIDN:AAA97013.1; | | | | | | | | | | | | |
| A: | Note: | the nucleotide sequence was submitted to the EMBL Data Library, August | | | | | | | | | | | | |
| R: | Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Rife | | | | | | | | | | | | | |
| .A.; | Rose, D.U.; Mau, B.; Shao, Y. | | | | | | | | | | | | | |
| Science | 277, | 1453-1462, 1997 | | | | | | | | | | | | |
| A: | Title: | The complete genome sequence of Escherichia coli K-12. | | | | | | | | | | | | |
| A: | Reference number: | A64720; MUID:97426617; PMID:9278503 | | | | | | | | | | | | |
| A: | Accession: | A65221 | | | | | | | | | | | | |
| A: | Status: | preliminary; nucleic acid sequence not shown; translation not shown | | | | | | | | | | | | |
| A: | Molecule type: | DNA | | | | | | | | | | | | |
| A: | Residues: | 1-557 <BLAT> | | | | | | | | | | | | |
| A: | Cross-references: | GB:AE000483; GB:U00096; NID:g2367351; PIDN:AAC77075.1; PID | | | | | | | | | | | | |
| A: | Experimental source: | strain K-12, substrain MG1655 | | | | | | | | | | | | |
| C: | Genetics: | | | | | | | | | | | | | |
| A: | Gene: | YjdB | | | | | | | | | | | | |
| C: | Superfamily: | Escherichia coli yidB protein | | | | | | | | | | | | |
| Query Match | 68.8%; | Score | 33; | DB | 2; | Length | 557; | | | | | | | |
| Best Local Similarity | 62.5%; | Pred.No. | 88; | | | | | | | | | | | |
| Matches | 5; | Conservative | 2; | Mismatches | 1; | Indels | 0; | Gaps | 0; | | | | | |
| Qy | 2 PHEITITAL 9 : Db | 347 PHQNVTAL 354 | | | | | | | | | | | | |
| RESULT 26 | | | | | | | | | | | | | | |
| H91265 | Hypothetical protein EC5096 [imported] - Escherichia coli (strain O157:H7, sub | | | | | | | | | | | | | |
| C: | Species: Escherichia coli | | | | | | | | | | | | | |
| C: | Date: | 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004 | | | | | | | | | | | | |
| C: | Accession: | H91265 | | | | | | | | | | | | |
| R: | Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; | | | | | | | | | | | | | |
| gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. | | | | | | | | | | | | | | |
| DNA Res. | 8, | 11-22, 2001 | | | | | | | | | | | | |
| A: | Title: | Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 | | | | | | | | | | | | |
| A: | Reference number: | A99629; MUID:21156231; PMID:11258796 | | | | | | | | | | | | |
| A: | Accession: | H91265 | | | | | | | | | | | | |
| A: | Status: | preliminary | | | | | | | | | | | | |
| A: | Molecule type: | DNA | | | | | | | | | | | | |
| A: | Residues: | 1-557 <HAY> | | | | | | | | | | | | |
| A: | Cross-references: | UNIPROT:Q8XEJ3; GB:RA000007; PIDN:BAB38519.1; PID:g1336457V | | | | | | | | | | | | |
| A: | Experimental source: | strain O157:H7, substrain RIMD 050952 | | | | | | | | | | | | |
| C: | Genetics: | | | | | | | | | | | | | |
| A: | Gene: | EC5096 | | | | | | | | | | | | |
| C: | Superfamily: | Escherichia coli yidB protein | | | | | | | | | | | | |
| Query Match | 68.8%; | Score | 33; | DB | 2; | Length | 557; | | | | | | | |
| Best Local Similarity | 62.5%; | Pred.No. | 88; | | | | | | | | | | | |
| Matches | 5; | Conservative | 2; | Mismatches | 1; | Indels | 0; | Gaps | 0; | | | | | |

```

QY      2 PHEITITAL 9
      || : |||
Db      347 PHQNTAL 354

RESULT 27
D87380
hypothetical protein CC1056 [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: D87380
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: D87380
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-613 <STO>
A:Cross-references: UNIPROT:Q9A9D2; GB:AE005673; NID:gl3422354; PIDN:AAK23040.1; GSPDB:G
C:Genetics:
A:Gene: CC1056

      Query Match      68.8%; Score 33; DB 2; Length 613;
      Best Local Similarity 66.7%; Pred. No. 99;
      Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 GPHETITAL 9
      || ||| ||
Db      44 GPSETLTGL 52

RESULT 28
S49788
probable membrane protein YIL092w - Yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein Y1910.04
C:Species: Saccharomyces cerevisiae
C>Date: 13-Jan-1995 #sequence_revision 10-Feb-1995 #text_change 09-Jul-2004
C:Accession: S49788
R:Connor, R.; Churcher, C.
submitted to the EMBL Data Library, November 1994
A:Reference number: S49786
A:Accession: S49788
A:Molecule type: DNA
A:Residues: 1-633 <CON>
A:Cross-references: UNIPROT:P40497; GB:Z47047; EMBL:Z46728; NID:g603997; PID:g763254; GS
C:Genetics:
A:Gene: MIPS:YIL092w
A:Cross-references: SGD:S0001354
A:Map position: 9L
C:Superfamily: Saccharomyces cerevisiae probable membrane protein YIL092w
C:Keywords: transmembrane protein
F:99-115/Domain: transmembrane #status predicted <TM>

      Query Match      68.8%; Score 33; DB 2; Length 633;
      Best Local Similarity 85.7%; Pred. No. 1e+02;
      Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 PHEITITA 8
      |||||
Db      566 PHETINA 572

RESULT 29
WMBEW6
capsid protein - human herpesvirus 1 (strain 17)
C:Species: human herpesvirus 1
C>Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
C:Accession: H30084
R:McGeoch, D.J.; Dalrymple, M.A.; Davison, A.J.; Dolan, A.; Frame, M.C.; McNab, D.; Perr
J. Gen. Virol. 69, 1531-1574, 1988

```

```

A:Title: The complete DNA sequence of the long unique region in the genome of herpes sim
A:Reference number: A30083; MUID:88274327; PMID:2839594
A:Accession: H30084
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-635 <MCG>
A:Cross-references: UNIPROT:P10210; GB:X14112; NID:gl944536; PIDN:CAA32318.1; PID:g59526;
C:Genetics:
A:Gene: UL26
C:Superfamily: varicella-zoster virus gene 33 protein
C:Keywords: capsid protein

      Query Match      68.8%; Score 33; DB 1; Length 635;
      Best Local Similarity 77.8%; Pred. No. 1e+02;
      Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GPHETITAL 9
      || ||| |||
Db      473 GTNETITAL 481

RESULT 30
D82452
anaerobic ribonucleoside-triphosphate reductase VCA0511 [imported] - Vibrio cholerae [str
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: D82452
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: D82452
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-706 <HEI>
A:Cross-references: UNIPROT:Q9KM77; GB:AE004381; GB:AE003853; NID:g9657902; PIDN:AAF96414
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VCA0511
A:Map position: 2
C:Superfamily: Escherichia coli oxygen-sensitive ribonucleoside-triphosphate reductase; c
ide-triphosphate reductase middle homology; rubredoxin homology
C:Keywords: iron; metalloprotein
F:644,647,662,665/Binding site: iron (Cys) #status predicted

      Query Match      68.8%; Score 33; DB 2; Length 706;
      Best Local Similarity 77.8%; Pred. No. 1.2e+02;
      Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 GPHETITAL 9
      || ||| |||
Db      492 GVHETITAL 500

RESULT 31
A64047
ribonucleoside-triphosphate reductase, oxygen-sensitive (EC 1.17.4.-) - Haemophilus infl
C:Species: Haemophilus influenzae
C>Date: 18-Aug-1995 #sequence_revision 19-Jan-1996 #text_change 09-Jul-2004
C:Accession: A64047
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: A64047
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-707 <TIGR>

```

A;Cross-references: UNIPROT:P43752; GB:U32693; NID:gl573021; PIDN:AAAC21751.1;
 C;Comment: This enzyme must be activated by the anaerobic ribonucleotide reductase activ-
 es peptide cleavage.
 C;Function:
 A;Description: catalyzes the reduction by reduced thioredoxin of a ribonucleoside tripho-
 A;Pathway: deoxyribonucleotide biosynthesis
 A;Note: this enzyme is different both from ribonucleoside-triphosphate reductase (EC 1.1.1
 nds iron and has a tyrosyl radical
 C;Superfamily: Escherichia coli oxygen-sensitive ribonucleoside-triphosphate reductase;
 C;Keywords: deoxyribonucleotide biosynthesis; iron; metalloprotein; oxidoreduc-
 F;96-279/Domain: oxygen-sensitive ribonucleoside-triphosphate reductase middle homology
 F;305-706/Domain: oxygen-sensitive ribonucleoside-triphosphate reductase middle homology
 F;641-671/Domain: rubredoxin homology #status atypical <RUB>
 F;644,647,663,666/Binding site: iron (Cys) #status predicted
 F;662/Active site: Gly (stable glycyl radical) #status predicted
 Query Match 68.8%; Score 33; DB 1; Length 707;
 Best Local Similarity 77.8%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GPHETITAL 9
 Db 494 GIHETINAL 502
 RESULT 32
 A47331
 ribonucleoside-triphosphate reductase, oxygen-sensitive (EC 1.17.4.-) - Escherichia coli
 N;Alternate names: anaerobic ribonucleotide reductase
 C;Species: Escherichia coli
 C;Date: 21-Sep-1993 #sequence revision 19-Jan-1996 #text_change 09-Jul-2004
 C;Accession: A47331; S56464; A65236
 R;Sun, X.; Harder, J.; Krook, M.; Jorvall, H.; Sjoberg, B.M.; Reichard, P.
 Proc. Natl. Acad. Sci. U.S.A. 90, 577-581, 1993
 A;Title: A possible glycine radical in anaerobic ribonucleotide reductase from Escherich
 A;Reference number: A47331; MUID:93133831; PMID:8421692
 A;Accession: A47331
 A;Molecule type: DNA; protein
 A;Residues: 1-256; 'R', 421-712 <SUN>
 A;Cross-references: UNIPROT:P28903; GB:L06097; NID:gl146968; PIDN:AA24226.1; PID:gl146970
 A;Note: sequence extracted from NCBI backbone (NCBIN:122818, NCBIP:122819)
 A;Note: parts of this sequence, including the amino end of the mature protein, were dete-
 R;Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
 Nucleic Acids Res. 23, 2105-2119, 1995
 A;Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.
 A;Reference number: S56314; MUID:95334362; PMID:7610040
 A;Accession: S56464
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-712 <BUR>
 A;Cross-references: EMBL:U14003; NID:gl263172; PIDN:AAA97135.1; PID:g537080
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co-
 A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A;Title: The complete genome sequence of Escherichia coli K-12.
 A;Reference number: A64720; MUID:97426617; PMID:9278503
 A;Accession: A65236
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-712 <BLAT>
 A;Cross-references: GB:AE000495; GB:U00096; NID:g2367361; PIDN:AACT77195.1; PID:gl190686;
 A;Experimental source: strain K-12, substrain MG1655
 C;Comment: This enzyme must be activated by the anaerobic ribonucleotide reductase activ-
 es peptide cleavage.
 C;Genetics:
 A;Gene: nrdd
 A;Map position: 96 min
 C;Complex: homodimer
 C;Function:
 A;Description: catalyzes the reduction by reduced thioredoxin of a ribonucleoside tripho-
 A;Pathway: deoxyribonucleotide biosynthesis

A;Note: this enzyme is different both from ribonucleoside-triphosphate reductase (EC 1.1.1;
 nds iron and has a tyrosyl radical
 C;Superfamily: Escherichia coli oxygen-sensitive ribonucleoside-triphosphate reductase;
 C;Keywords: deoxyribonucleotide biosynthesis; iron; metalloprotein; oxidoreduc-
 F;96-279/Domain: oxygen-sensitive ribonucleoside-triphosphate reductase middle homology
 F;305-706/Domain: oxygen-sensitive ribonucleoside-triphosphate reductase middle homology
 F;641-671/Domain: rubredoxin homology #status atypical <RUB>
 F;644,647,662,665/Binding site: iron (Cys) #status predicted
 F;681/Active site: Gly (stable glycyl radical) #status predicted
 Query Match 68.8%; Score 33; DB 1; Length 712;
 Best Local Similarity 77.8%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GPHETITAL 9
 Db 493 GIHETINAL 501
 RESULT 33
 AC1058
 ribonucleoside-triphosphate reductase (EC 1.17.4.2) - Salmonella enterica subsp. enterica
 C;Species: Salmonella enterica subsp. enterica serovar Typhi
 A;Note: this species has also been called Salmonella typhi
 C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C;Accession: AC1058
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
 th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moule, S.; O'Garra, P.
 Nature 413, 848-852, 2001
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar
 A;Reference number: AB0502; MUID:21534947; PMID:11677608
 A;Accession: AC1058
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-712 <PAR>
 A;Cross-references: GB:AL513382; PIDN:CAD06912.1; PID:gl6505560; GSPDB:GN00176
 C;Genetics:
 A;Gene: nrdd
 C;Superfamily: Escherichia coli oxygen-sensitive ribonucleoside-triphosphate reductase;
 C;Keywords: iron; metalloprotein; oxidoreductase
 F;644,647,662,665/Binding site: iron (Cys) #status predicted
 Query Match 68.8%; Score 33; DB 2; Length 712;
 Best Local Similarity 77.8%; Pred. No. 1.2e+02;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GPHETITAL 9
 Db 493 GIHETINAL 501
 RESULT 34
 G91280
 anaerobic ribonucleoside-triphosphate reductase [imported] - Escherichia coli (strain O1
 C;Species: Escherichia coli
 C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
 C;Accession: G91280
 R;Hayaishi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
 Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno-
 A;Reference number: A99629; MUID:21156231; PMID:11258796
 A;Accession: G91280
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-712 <HAY>
 A;Cross-references: UNIPROT:Q8XCE2; GB:BA000007; PIDN:BA38638.1; PID:gl3364692; GSPDB:G
 A;Experimental source: strain O157:H7, substrain RIMD 0509952
 C;Genetics:

A:Gene: EC85215
C:Superfamily: Escherichia coli oxygen-sensitive ribonucleoside-triphosphate reductase;
ide-triphosphate reductase middle homology; rubredoxin homology
C:Keywords: iron; metalloprotein
F:644,647,662,665/Binding site: iron (Cys) #status predicted

Query Match 68.8%; Score 33; DB 2; Length 712;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPHETITAL 9
| | | | | | |
Db 493 GIHETINAL 501

RESULT 35
G86121
A:Gene: anaerobic ribonucleoside-triphosphate reductase [imported] - Escherichia coli (strain O1
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: G86121
R:Perina, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: G86121
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-712 <STO>
A:Cross-references: UNIPROT:O8XCE2; GB:AE005174; NID:gl2519242; PIDN:AG59435.1; GSPDB:G
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: nrdd
C:Superfamily: Escherichia coli oxygen-sensitive ribonucleoside-triphosphate reductase;
ide-triphosphate reductase middle homology; rubredoxin homology
C:Keywords: iron; metalloprotein
F:644,647,662,665/Binding site: iron (Cys) #status predicted

Query Match 68.8%; Score 33; DB 2; Length 712;
Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPHETITAL 9
| | | | | | |
Db 493 GIHETINAL 501

RESULT 36
AG0419
A:Gene: ribonucleoside-triphosphate reductase (EC 1.17.4.2) [imported] - Yersinia pestis (strain
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AG0419
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AG0419
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-712 <KUR>
A:Cross-references: UNIPROT:Q8ZBG2; GB:AL590842; PIDN:CAC92683.1; PID:g15981378; GSPDB:G
C:Genetics:
A:Gene: nrdd
C:Superfamily: Escherichia coli oxygen-sensitive ribonucleoside-triphosphate reductase;
ide-triphosphate reductase middle homology; rubredoxin homology
C:Keywords: iron; metalloprotein; oxidoreductase
F:644,647,662,665/Binding site: iron (Cys) #status predicted

Query Match 68.8%; Score 33; DB 2; Length 712;

Best Local Similarity 77.8%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPHETITAL 9
| | | | | | |
Db 492 GIHETINAL 500

RESULT 37
S54595
A:Gene: probable membrane protein YMR288w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein YMR288w
C:Species: Saccharomyces cerevisiae
C:Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S54595
R:Pearson, D.; Bowman, S.
submitted to the EMBL Data Library, May 1995
A:Reference number: S54582
A:Accession: S54595
A:Molecule type: DNA
A:Residues: 1-971 <PEA>
A:Cross-references: UNIPROT:P49955; EMBL:Z49704; NID:g825540; PID:g825554; GSPDB:GN00013;
A:Experimental source: strain AB972
C:Genetics:
A:Gene: SGD:HS155; MIPS:YMR288w
A:Cross-references: SGD:S0004901
A:Map position: 13R
C:Keywords: transmembrane protein
F:733-349/Domain: transmembrane #status predicted <TM1>
F:777-793/Domain: transmembrane #status predicted <TM2>

Query Match 68.8%; Score 33; DB 2; Length 971;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPHETITAL 9
| | | | | | |
Db 758 GPHDVLVAL 766

RESULT 38
T30544
A:Gene: major surface glycoprotein - Pneumocystis carinii (fragment)
C:Species: Pneumocystis carinii
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 15-Jun-2001
C:Accession: T30544
R:Mei, Q.; Turner, R.E.; Sorial, V.; Klivington, D.; Angus, C.W.; Kovacs, J.A.
Infect. Immun. 66, 4268-4273, 1998
A:Title: Characterization of major surface glycoprotein genes of human Pneumocystis carii
A:Reference number: Z17905; MUID:98380374; PMID:9712777
A:Accession: T30544
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1008 <MEI>
A:Cross-references: EMBL:AF033212; NID:g3560520; PID:g3560521; PIDN:AAC34975.1
C:Genetics:
A:Gene: MSG
C:Superfamily: Pneumocystis carinii major surface glycoprotein MSG100

Query Match 68.8%; Score 33; DB 2; Length 1008;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PHETIT 7
| | | | | | |
Db 920 PHETITV 925

RESULT 39
T30542
A:Gene: major surface glycoprotein - Pneumocystis carinii (fragment)
C:Species: Pneumocystis carinii
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 15-Jun-2001

A;Gene: T30542
C;Superfamily: ictaluriid herpesvirus 1 hypothetical protein ORF56
R;Mei, Q.; Turner, R.E.; Sorial, V.; Klivington, D.; Angus, C.W.; Kovacs, J.A.
Infect. Immun. 66, 4268-4273, 1998
A;Title: Characterization of major surface glycoprotein genes of human Pneumocystis carinii
A;Reference number: Z17905; MUID:98380374; PMID:9712777
A;Accession: T30542
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1017 <MEI>
A;Cross-references: EMBL:AF033210; NID:G3560516; PID:G3560517; PIDN:AAC34973.1
C;Genetics:
A;Gene: MSG
C;Superfamily: Pneumocystis carinii major surface glycoprotein MSG100

Query Match 68.8%; Score 33; DB 2; Length 1017;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PHETIT 7
Db 912 PHETVT 917
|||||

RESULT 40
T30543
major surface glycoprotein - Pneumocystis carinii (fragment)
C;Species: Pneumocystis carinii
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 15-Jun-2001
C;Accession: T30543
R;Mei, Q.; Turner, R.E.; Sorial, V.; Klivington, D.; Angus, C.W.; Kovacs, J.A.
Infect. Immun. 66, 4268-4273, 1998
A;Title: Characterization of major surface glycoprotein genes of human Pneumocystis carinii
A;Reference number: Z17905; MUID:98380374; PMID:9712777
A;Accession: T30543
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1022 <MEI>
A;Cross-references: EMBL:AF033211; NID:G3560518; PID:G3560519; PIDN:AAC34974.1
C;Genetics:
A;Gene: MSG
C;Superfamily: Pneumocystis carinii major surface glycoprotein MSG100

Query Match 68.8%; Score 33; DB 2; Length 1022;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 PHETIT 7
Db 915 PHETVT 920
|||||

RESULT 41
C36792
hypothetical protein ORF56 - ictaluriid herpesvirus 1 (strain auburn 1)
C;Species: ictaluriid herpesvirus 1
A;Note: host Ictalurus punctatus (channel catfish)
C;Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 09-Jul-2004
C;Accession: C36792
R;Davison, A.J.
submitted to GenBank, January 1992
A;Description: Channel catfish virus: a new type of herpesvirus.
A;Reference number: A36804
A;Accession: C36792
A;Molecule type: DNA
A;Residues: 1-1179 <DAV>
A;Cross-references: UNIPROT:Q00099; GB:M75136; NID:G331209; PIDN:AAA88159.1; PID:G331266
R;Davison, A.J.
Virology 186, 9-14, 1992
A;Title: Channel catfish virus: a new type of herpesvirus.
A;Reference number: A39447; MUID:92087490; PMID:1727613
A;Contents: annotation
A;Note: neither protein nor nucleic acid sequence is given
C;Genetics:

A;Gene: 56
C;Superfamily: ictaluriid herpesvirus 1 hypothetical protein ORF56
Query Match 68.8%; Score 33; DB 2; Length 1179;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPHEITIT 7
Db 828 GPHGTIT 834
|||||

RESULT 42
MWXR31
lambda 3 protein - reovirus type 1 (strain Lang)
N;Alternate names: minor core protein
C;Species: reovirus type 1
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: A30121
R;Wiener, J.R.; Joklik, W.K.
Virology 169, 194-203, 1989
A;Title: The sequences of the reovirus serotype 1, 2, and 3 L1 genome segments and analysis
A;Reference number: A94390; MUID:89163254; PMID:2922925
A;Accession: A30121
A;Molecule type: genomic RNA
A;Residues: 1-1267 <WIE>
A;Cross-references: UNIPROT:P17376; GB:M24734; NID:G499863
A;Note: this sequence, which matches the sequence attributed to type 1 in Fig. 2, matches the translations in entries REO1LAM3P and REO3LAM3P now differ only by the sequence correction
C;Comment: See also PIR:MWXR33.
C;Genetics:
A;Map position: segment L1
C;Superfamily: reovirus lambda 3 protein
C;Keywords: core protein

Query Match 68.8%; Score 33; DB 1; Length 1267;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PHETITA 8
Db 105 PHETLTS 111
|||||

RESULT 43
MWXR32
lambda 3 protein - reovirus type 2 (strain D5/Jones)
N;Alternate names: minor core protein
C;Species: reovirus type 2
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: B30121
R;Wiener, J.R.; Joklik, W.K.
Virology 169, 194-203, 1989
A;Title: The sequences of the reovirus serotype 1, 2, and 3 L1 genome segments and analysis
A;Reference number: A94390; MUID:89163254; PMID:2922925
A;Accession: B30121
A;Molecule type: genomic RNA
A;Residues: 1-1267 <WIE>
A;Cross-references: UNIPROT:P17377; GB:M31057; NID:G499865; PIDN:AAA47245.1; PID:G499866
C;Genetics:
A;Map position: segment L1
C;Superfamily: reovirus lambda 3 protein
C;Keywords: core protein

Query Match 68.8%; Score 33; DB 1; Length 1267;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PHETITA 8
Db 105 PHETLTS 111
|||||

RESULT 44

MXR33

lambda 3 protein - reovirus type 3 (strain Dearing)

N:Alternate names: minor core protein

C:Species: reovirus type 3

C>Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004

C:Accession: C30121

R:Wiener, J.R.; Joklik, W.K.

Virology 169, 194-203, 1989

A:Title: The sequences of the reovirus serotype 1, 2, and 3 L1 genome segments and analysis

A:Reference number: A94390; MUID:89163254; PMID:2922925

A:Accession: C30121

A:Molecule type: genomic RNA

A:Residues: 1-1267 <WIR>

A:Cross-references: UNIPROT:P17378; GB:M31058; NID:9499867; GB:M24734; NID:9499863; PIDN

N:Note: This sequence, which matches the sequence attributed to type 3 in Fig. 2, matches

ntries REO11AM3P and REO31AM3P now differ only by the sequence correction apparently mad

C:Comment: See also PIR:MXR31.

C:Genetics:

A:Map position: segment L1

A:Superfamily: reovirus lambda 3 protein

C:Keywords: core protein

Query Match 68.8%; Score 33; DB 1; Length 1267;
 Best Local Similarity 71.4%; Pred. No. 2.2e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 PHETITA 8

|||||:

Db 105 PHETLTS 111

RESULT 45

T38353

serine hydroxymethyltransferase - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: T38353

R:Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.

submitted to the EMBL Data Library, August 1995

A:Reference number: Z21787

A:Accession: T38353

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-467 <MUR>

A:Cross-references: UNIPROT:O13972; EMBL:Z98601; PIDN:CAB11269.1; GSPDB:GN00066; SPDB:SF

A:Experimental source: strain 972h-; cosmid C24C9

C:Genetics:

A:Gene: SPDB:SPAC24C9.12c

A:Map position: 1

C:Superfamily: serine/glycine hydroxymethyltransferase

Query Match 67.7%; Score 32.5; DB 2; Length 467;
 Best Local Similarity 80.0%; Pred. No. 93;
 Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GPH-ETITAL 9

|||||

Db 288 GPHNHTITAL 297

RESULT 46

T37918

serine hydroxymethyltransferase - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004

C:Accession: T37918

R:Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.; Wood, V.

submitted to the EMBL Data Library, December 1995

A:Reference number: Z21754

A:Accession: T37918

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-472 <CON>

A:Cross-references: UNIPROT:Q10104; EMBL:Z68198; PIDN:CAA92384.1; GSPDB:GN00066; SPDB:SP1

A:Experimental source: strain 972h-; cosmid c18G6

C:Genetics:

A:Gene: SPDB:SPAC18G6.04c

A:Map position: 1

C:Superfamily: serine/glycine hydroxymethyltransferase

Query Match 67.7%; Score 32.5; DB 2; Length 472;
 Best Local Similarity 80.0%; Pred. No. 94;
 Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GPH-ETITAL 9

|||||

Db 294 GPHNHTITAL 303

RESULT 47

A42241

glycine hydroxymethyltransferase (EC 2.1.1.2.1), cytosolic - Neurospora crassa

N:Alternate names: serine hydroxymethyltransferase

C:Species: Neurospora crassa

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: A42241

R:McClung, C.R.; Davis, C.R.; Page, K.M.; Denome, S.A.

Mol. Cell. Biol. 12, 1412-1421, 1992

A:Title: Characterization of the formate (for) locus, which encodes the cytosolic serine

A:Reference number: A42241; MUID:92195285; PMID:1532227

A:Accession: A42241

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-479 <MCC>

A:Cross-references: UNIPROT:P34898; GB:M81918

C:Superfamily: serine/glycine hydroxymethyltransferase

C:Keywords: cytosol; phosphoprotein; pyridoxal phosphate; transferase

P:249/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 67.7%; Score 32.5; DB 1; Length 479;
 Best Local Similarity 80.0%; Pred. No. 95;
 Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 GPH-ETITAL 9

|||||

Db 294 GPHNHTITAL 303

RESULT 48

T03782

probable lipid transfer protein - rice

C:Species: Oryza sativa (rice)

C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C:Accession: T03782

R:Vignols, F.; Lund, G.; Pham, S.; Tremousaygue, D.; Grelllet, F.; Kader, J.; Puidomec

Gene 142, 265-270, 1994

A:Title: Characterization of a rice gene coding for a lipid transfer protein.

A:Reference number: Z15081; MUID:94252578; PMID:8194762

A:Accession: T03782

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-117 <VIG>

A:Cross-references: UNIPROT:Q42999; EMBL:Z23271; NID:9510336; PIDN:CAA80809.1; PID:951033

A:Experimental source: cv. IR36

C:Genetics:

A:Introns: 115/3

C:Superfamily: phospholipid transfer protein

Query Match 66.7%; Score 32; DB 2; Length 117;
 Best Local Similarity 55.6%; Pred. No. 25;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPHETITAL 9

|||||:

Db 20 GPHTTMAAI 28

RESULT 49

T02042

lipid transfer protein LPT II - rice

C;Species: Oryza sativa (rice)

C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 09-Jul-2004

C;Accession: T02042

R;Lee, M.C.; Kim, C.S.; Eun, M.Y.

submitted to the EMBL Data Library, August 1997

A;Description: Isolation and characterization of lipid transfer protein from rice.

A;Reference number: Z14508

A;Accession: T02042

A;Status: preliminary; translated from GE/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-118 <LEE>

A;Cross-references: UNIPROT:O22483; EMBL:AF017359; NID:g2407272; PIDN:AAB70539.1; PID:g2

A;Experimental source: strain Milyang 23

C;Superfamily: phospholipid transfer protein

Query Match 66.7%; Score 32; DB 2; Length 118;
Best Local Similarity 55.6%; Pred.No. 25;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPHTTITAL 9

Db 20 GPHTTMAAI 28

RESULT 50

T03300

probable lipid transfer protein precursor - rice

C;Species: Oryza sativa (rice)

C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004

C;Accession: T03300

R;Li, G.

submitted to the EMBL Data Library, July 1995

A;Reference number: Z14895

A;Accession: T03300

A;Status: preliminary; translated from GE/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-118 <LIA>

A;Cross-references: UNIPROT:Q42978

A;Experimental source: strain Guang-lu-ai 4, shoot

C;Genetics:

A;Gene: Ltp2

C;Superfamily: phospholipid transfer protein

F;1-26/Domain: signal sequence #status predicted <SIG>

F;27-118/Product: lipid transfer protein #status predicted <MAT>

Query Match 66.7%; Score 32; DB 2; Length 118;
Best Local Similarity 55.6%; Pred.No. 25;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPHTTITAL 9

Db 20 GPHTTMAAI 28

Search completed: July 27, 2005, 12:42:07

Job time : 56 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 27, 2005, 12:03:22 ; Search time 40 Seconds
(without alignments)
538.814 Million cell updates/sec

Title: US-10-623-429-9_COPY_404_627
Perfect score: 1237
Sequence: 1 AIAADROAGGLPAAAGDHGI.....ALVNASSAAHVNVDTPARAAD 224

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------|---------------------------------|
| 1 | 670.5 | 54.2 | 635 | 1 WMBE6 | capsid protein - h |
| 2 | 221.5 | 17.9 | 522 | 2 S52216 | viral proteinase - rabies virus |
| 3 | 215 | 17.4 | 699 | 2 T05225 | extensin homolog F |
| 4 | 211 | 17.1 | 646 | 1 W2BEC8 | 68.6K capsid prote |
| 5 | 206 | 16.7 | 727 | 2 C84534 | hypothetical prote |
| 6 | 204 | 16.5 | 620 | 2 S06733 | hydroxyproline-ric |
| 7 | 200 | 16.2 | 464 | 2 S22697 | extensin - Volvox |
| 8 | 198 | 16.0 | 760 | 2 T08291 | extensin homolog T |
| 9 | 196 | 15.8 | 929 | 2 C96623 | hypothetical prote |
| 10 | 195.5 | 15.8 | 599 | 2 T10798 | pherophorin-S - Vo |
| 11 | 195 | 15.8 | 134 | 2 JC5572 | proline-rich prote |
| 12 | 194.5 | 15.7 | 485 | 2 A33647 | sulfated surface g |
| 13 | 193 | 15.6 | 847 | 2 F94531 | hypothetical prote |
| 14 | 191.5 | 15.5 | 217 | 2 T09965 | extensin CYC17 pre |
| 15 | 190.5 | 15.4 | 551 | 2 S57447 | HPBRII-7 protein - |
| 16 | 190.5 | 15.4 | 647 | 2 T42579 | capsid protein 35 |
| 17 | 190 | 15.4 | 464 | 2 A47655 | spliceosome-associ |
| 18 | 190 | 15.4 | 1188 | 2 S49915 | extensin-like prot |
| 19 | 188.5 | 15.2 | 428 | 2 E71415 | probable coll wall |
| 20 | 187.5 | 15.2 | 839 | 2 T04859 | extensin homolog F |
| 21 | 187 | 15.1 | 368 | 2 C29356 | hydroxyproline-ric |
| 22 | 187 | 15.1 | 907 | 2 E96636 | hypothetical prote |
| 23 | 186.5 | 15.1 | 997 | 2 T28872 | hypothetical prote |
| 24 | 186 | 15.0 | 1006 | 2 G86292 | extensin-like prot |
| 25 | 185 | 15.0 | 242 | 2 S54156 | hypothetical prote |
| 26 | 185 | 15.0 | 416 | 2 T34279 | probable pro kinas |
| 27 | 185 | 15.0 | 760 | 2 F86387 | extensin class I (|
| 28 | 184.5 | 14.9 | 132 | 2 S14970 | hypothetical prote |
| 29 | 184.5 | 14.9 | 1018 | 2 T43168 | hypothetical prote |

hypothetical prote
probable proline-r
hypothetical proce
immediate-early pr
extensin-like cell
hypothetical prote
C-terminal domain-
extensin-like prot
extensin precursor
pistil extensin-li
chitinase (EC 3.2.
unknown protein (i
hydroxyproline-ric
nodulin precursor
hydroxyproline-ric
Wiskott-Aldrich sy

30 184.5 14.9 1259 2 T16038
31 183 14.8 191 2 F84522
32 183 14.8 222 2 H96711
33 183 14.8 1460 1 EDBEIF
34 182.5 14.8 214 2 T10737
35 182.5 14.8 667 2 T17221
36 182.5 14.8 1048 2 T31425
37 180.5 14.6 280 2 T11671
38 180 14.6 322 2 S25299
39 180 14.6 393 2 PQ0479
40 180 14.6 439 2 S51939
41 180 14.6 1201 2 G86441
42 179.5 14.5 163 2 A29356
43 179.5 14.5 309 2 S08343
44 179.5 14.5 369 2 S20500
45 179.5 14.5 440 2 JC7807

RESULT 1
WMBE6
capsid protein - human herpesvirus 1 (strain 17)
C:Species: human herpesvirus 1
C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
C:Accession: H30084
R:McGeoch, D.J.; Dalrymple, M.A.; Davison, A.J.; Dolan, A.; Frame, M.C.; McNab, D.; Peri
J. Gen. Virol. 69, 1531-1574, 1988
A:Title: The complete DNA sequence of the long unique region in the genome of herpes sim
A:Reference number: A30083; MUID:88274327; PMID:2839594
A:Accession: H30084
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-635 <MCG>
A:Cross-references: UNIPROT:P10210; GB:X14112; NID:G1944536; PIDN:CAA32318.1; PID:G595526
C:Genetics:
A:Gene: UL26
C:Superfamily: varicella-zoster virus gene 33 protein
C:Keywords: capsid protein

ALIGNMENTS

Query Match 54.2%; Score 670.5; DB 1; Length 635;
Best Local Similarity 63.4%; Pred. No. 2.5e-33;
Matches 144; Conservative 12; Mismatches 64; Indels 7; Gaps 4;

QY 1 AIAADROAGGLPAAAGDHGIRGSAKRREHEVEQPEYDCGRDEPRDRFFYPYGEARPEPRP 60
DB 403 AIAADROAGGQP-AAGDFGVRGSGKRRYEAGPSYCDQDEPDADYPYPGEARGAPRG 461
QY 61 VDSRAARQASGPHETITATLVGAVTSLOQLAHMARHAPYGPYPYPVGHPHADTE- 119
DB 462 VDSRAARHSPTNETITATLVGAVTSLOQLAHMARHAPYGPYPYPVGHPHADTE- 521
QY 178 PPPPPGTPPPPAALPOEAPGAGALVNASSAAHVNVDTPARAAD 224
DB 579 RAFLTEPAFPATGSPQPEASNAEAGALVNASSAAHVNVDTPARAAD 625

RESULT 2

S52216
viral proteinase - rabies virus
C:Species: rabies virus
C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Aug-1998
C:Accession: S52216
R:Camacho, A.; Tabaro, E.
submitted to the EMBL Data Library, June 1994
A:Reference number: S52215
A:Accession: S52216
A:Status: preliminary


```
Qy 45 RDP--PYPGEARPEPR-----PVDERRAARQASGPHETTALVGAVTSLQQLAHMRA 96
Db 404 RPVHKPQPKES--QPNDPVNQSPVKFRSSPPPPQOPH-----HHVHSPP 448
Qy 97 RTHAPYGPYPV---GPYHHPHADTETPAQPPY-----PAKAVYLLPPP--- 137
Db 449 PASSP-PTSPPVHSTPSPVHKPQPKESQPNDDYDQSPVKFRSSPPPPVHSPSPSP 507
Qy 138 HIAPGGLSCAVPPPSY---PPVAVTPGAPPLHQ-PSPAHAHPP-----PPPGGTPP 188
Db 508 KSPPPPPVSPPPPPVSPPPPPVSPPPPPVSPPPPPVSPPPPPVSPPPPPVSPPP 567
Qy 189 PAASLPQP 196
Db 568 PPVHSPP 575

RESULT 6
S06733
hydroxyproline-rich glycoprotein precursor - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C:Accession: S06733
Genes Dev. 3, 1639-1646, 1989
R:Keller, B.; Lamb, C.J.
A:Title: Specific expression of a novel cell wall hydroxyproline-rich glycoprotein gene
A:Reference number: S06733; MUID:90128263; PMID:2612909
A:Accession: S06733
A:Molecule type: DNA
A:Residues: 1-620 <KEL>
A:Cross-references: UNIPROT:P13983; EMBL:X13885; NID:g19866; PID:g19867
C:Superfamily: hydroxyproline-rich glycoprotein
C:Keywords: Glycoprotein

Query Match 16.5%; Score 204; DB 2; Length 620;
Best Local Similarity 27.7%; Pred. No. 1.9e-05;
Matches 65; Conservative 21; Mismatches 81; Indels 68; Gaps 10;

Qy 28 RHEVQPEYD-----CGRDEPRDF-PVPGEARPEPRPVDERRAARQASGPHETTAL 80
Db 257 RQOPQPTSPPPPPAYASQPSPTSPPTSPPTSPPTSPPTSPPTSPPTSPPTSPPT 315
Qy 81 VGAVTSLQQLAHMRAHAP-----YGPYPV-----GPYHHPHADT----- 118
Db 316 ----TFSPPPAYSPPTSPPTSPPTSPPTSPPTSPPTSPPTSPPTSPPTSPPT 371
Qy 119 -----ETPAQPPY-----PAKAVYLLPPP-----HIAPGGLP 146
Db 372 PPPSPPPPSFSPPTSPPTSPPTSPPTSPPTSPPTSPPTSPPTSPPTSPPTSPPT 431
Qy 147 SCAVPPPSY-PPVAVTPGAPPLHQ-PSPAHAHPPPPPPGTPPPPAASLPQPEAP 199
Db 432 TYSPPPPAYSPPTSPPTSPPTSPPTSPPTSPPTSPPTSPPTSPPTSPPTSPPT 486

RESULT 7
S22697
extensin - Volvox carteri (fragment)
C:Species: Volvox carteri
C>Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C:Accession: S22697; S21006
R:Ertl, H.; Hallmann, A.; Wenzl, S.; Sumper, M.
EMBO J. 11, 2055-2062, 1992
A:Title: A novel extensin that may organize extracellular matrix biogenesis in Volvox ca
A:Reference number: S22697; MUID:92289669; PMID:1600938
A:Accession: S22697
A:Molecule type: mRNA
A:Residues: 1-464 <HAL>
A:Cross-references: UNIPROT:Q41645; EMBL:X65165; NID:g21991; PID:CAA46283.1; PID:g21992
C:Keywords: glycoprotein

Query Match 16.2%; Score 200; DB 2; Length 464;
Best Local Similarity 33.1%; Pred. No. 2.6e-05;
```

```
Matches 57; Conservative 10; Mismatches 71; Indels 34; Gaps 7;

Qy 48 PYPGEARPEPRPVDERRAARQASGPHETTALVGAVTSLQQLAHMRAHAPYGPYP 107
Db 232 PPPARVSSSPPPATRRITSPSPVLTA-----SPPLPKTSP-PPPR 277
Qy 108 VGPVHHPHADTETPAQPPRY-----PAKAVYLLPPPPIAP-----PGPPLSG-----AVP 151
Db 278 VPSPPPPPVAVSPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 337
Qy 152 PPSPPPPVAVTPGAPPLHQPSPAH--AHPPPPPP--GTPPPPAASLPQPEAP 199
Db 338 PPSPPPPPPSPPPPPSPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 389

RESULT 8
T06291
extensin homolog T9E8.80 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004
C:Accession: T06291
R:Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Schuel
submitted to the Protein Sequence Database, April 1999
A:Reference number: Z15588
A:Accession: T06291
A:Molecule type: DNA
A:Residues: 1-760 <BEV>
A:Cross-references: UNIPROT:Q9TOK5; EMBL:AL049608
A:Experimental source: cultivar Columbia; BAC clone T9E8
C:Genetics:
A:Map position: 4
A:Note: T9E8.80

Query Match 16.0%; Score 198; DB 2; Length 760;
Best Local Similarity 42.6%; Pred. No. 5.2e-05;
Matches 46; Conservative 3; Mismatches 47; Indels 12; Gaps 3;

Qy 102 YGPVPPVGPYHHPHADTETPAQPPRYPAKAVYLLPPPPIAPGPP--LSGAVPPSPYPPVA 159
Db 449 YSPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 508
Qy 160 VTPGAPPLHQ-----PSPAH-----AHPPPPPPGTPPPPAASLPQPE 197
Db 509 VYSPPPPPVYSSPPPPPPSPAPTPVCTRPPPPPHSPPPPPQFSPPPE 556

RESULT 9
C36623
hypothetical protein F23H11.22 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: C36623
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: C36623
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-929 <STO>
A:Cross-references: UNIPROT:Q9XIE0; GB:AE005173; NID:g5080823; PIDN:AAD39332.1; GSPDB:G
C:Genetics:
A:Map position: 1

Query Match 15.8%; Score 196; DB 2; Length 929;
```

| | |
|---|--|
| Best Local Similarity 27.1%, Pred. No. 8.2e-05; | |
| Matches 67; Conservative 22; Mismatches 96; Indels 62; Gaps 10; | |
| Qy | 13 AAAGDHGIRGSAKRRRHEVEQPE-----YDCGRDEPDRDRP-----YYPG 52 |
| Db | 202 SAGSDYGGGGKQSQKFOAPGGGSPFSQIHSGGHSPLPLDPGQFTAGNASFPS 261 |
| Qy | 53 EARPEPRPVDSRRRAARQASGHETITALVG-----AVTSL---QOELAHMRARTHAPYGP 104 |
| Db | 262 STQPPPGQYMAGNASFSSSTPLPPGQYMAGNAPSSSTPLPPGQYPAVNAQLSTSAFVP 321 |
| Qy | 105 YPPVGPYHHPHADTETPAQPRYPKAVYLP-----PPHTAPPG 143 |
| Db | 322 LFP--GQTVANNAPESTSTQPVSLP--PGQYMPGNAAALSASTLTPGQFTTANAPP--APPG 377 |
| Qy | 144 PPLSGAVPPSPYPVAVTPGPAPPLHQPSPAHAHPPPPPPPG-----PTPSPAAASLPQPE 197 |
| Db | 378 PANQTSPPPPPPPSAAAPPPPPPPKKGPA---APPPPPPPKKGAGGPPPPPPMSKKGPPK 434 |
| Qy | 198 APGAEG 204 |
| Db | 435 PGNPKG 441 |

RESULT 10
Ti0798
pherophorin-S - Volvox carteri
C/Species: Volvox carteri
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C/Accession: Ti0798
R/Godl, K.; Hallmann, A.; Wenzl, S.; Sumper, M.
EMBO J. 16, 25-34, 1997
A/Title: Differential targeting of closely related ECM-glycoproteins: The perophorin f
A/Reference number: Z17154; MUID:97162277; PMID:9009264
A/Accession: Ti0798
A/Status: preliminary; translated from GE/EMBL/DBDB
A/Molecule type: mRNA
A/Residues: 1-599 <GOD>
A/Cross-references: UNIPROT:P93797; EMBL:Y07752; NID:g1655698; PIDN:CAA69032.1; PID:g165
A/Experimental source: strain HK 10; sub species Nagariensis
A/Note: In contrast to the other perophorins, perophorin-S is targeted to the cell-fre
C/Keywords: extracellular matrix; glycoprotein; pheromone

[illegible]

```

RESULT 11
JC5572
proline-rich protein P-B1 precursor - human
C/Species: Homo sapiens (man)
C/Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 09-Jul-2004
C/Accession: JC5572
R:Risemura, S.; Saitoh, E.
J. Biochem. 121, 1025-1030, 1997
A/Title: Nucleotide sequence of gene PBI encoding a protein homologous to salivary prolin
A/Reference number: JC5572; MUID:98014462; PMID:9354371
A/Accession: JC5572
A:Molecule type: DNA
A/Residues: 1-134 <ISE>
A/Cross-references: UNIPROT:Q99954; DBJ:D89501; NID:gl854451; PID:BAAL13971.1; PID:gl85
C/Comment: This protein plays roles in the maintenance of teeth by inhibiting crystal gr
tion from the digestive organs.
C/Genetics:

```

```

A; Introns: 18/3
C; Superfamily: proline-rich peptide P-B
F; 1-22/Domain: signal sequence #status predicted <SIG>
F; 23-134/Product: proline-rich protein P-B1 #status predicted <MAT>
F; 23-45/Domain: amino-terminal propeptide #status predicted <ATP>
F; 46-58, 59-71, 72-84, 85-97, 98-112/Region: repeat
F; 113-134/Domain: carboxyl-terminal peptide #status predicted <CTP>

Query Match          15.8%; Score 195; DB 2; Length 134;
Best Local Similarity 41.7%; Pred. No. 1,7e-05;
Matches 43; Conservative 7; Mismatches 37; Indels 16; Gaps 5;

Qy 101 PVGPPVPGVHHPHADTETPAQPPRYPAKAVLPPPHIAPGPPSLGAVPPSPVPPVA- 159
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 26 PRGFPYP-GPL-----APPPPRFPFGTGVPPHPHPYPGYP---GRFPPLSLPPYGP 73

Qy 160 --VTGPAAPLHQPSPAHAPHPPPPPGPTPTPPAASLPQPEAPG 200
      :|||: ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 74 GRIPSPPPP-YGQGRIOQSHSLPFPYGGVYQPPSPQRPYPYPG 115
      :|||: ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

RESULT 12
A33647
sulfated surface glycoprotein 185 - Volvox carteri
C/Species: Volvox carteri
C/Date: 11-Apr-1990 #sequence_revision 11-Apr-1990 #text_change 09-Jul-2004
C/Accession: A33647
J. Cell Biol. 109, 3493-3501, 1989
R;Ertl, H.; Mengele, R.; Wenzl, S.; Engel, J.; Sumper, M.
A/Title: The extracellular matrix of Volvox carteri: molecular structure of the cellular
A/Reference number: A33647; MUID:90094551; PMID:2689458
A/Accession: A33647
A/Status: preliminary
A/Molecule type: mENA
A/Residues: 1-485 <ERT>
A/Cross-references: UNIPROT:P21997; GB:X51616; NID:g21999; PIDN:CAA35953.1; PID:g1405821
C/Keywords: glycoprotein

```

Query Match      15.7%; Score 194.5; DB 2; Length 485;
Best Local Similarity 40.4%; Pred. No. 5.7e-05;
Matches 44; Conservative 9; Mismatches 35; Indels 21; Gaps 6;

Qy      101 PYGYP----PVGYPYHHADTETPAQP--PRPTAKAVYLEPPPHIAPGPPPLSGAVPPPSY 155
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      219 PIGAPANNPLPPSPQPTASSRPPPPSPRRPSP-----PPSPSPPPPP-----PPPPP 269

Qy      156 PPVATPGAPAPLHPGSAHAHPPPPPPGCTTP-----PAASLPQPPAP 199
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      270 PPPPPPPPPPP--PPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 316

```

RESULT 13

F96531
hypothetical protein F13P21.7 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: F96531
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: F96531
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-847 <STO>
A:Cross-references: UNIPROT:Q9XIB6; GB:AE005173; NID:g54330752; PIDN:AA043152.1; GSPDB:GN

C:Genetics:
A:Gene: F13F21.7
A:Map position: 1

Query Match 15.6%; Score 193; DB 2; Length 847;
Best Local Similarity 30.7%; Pred. No. 0.00011;
Matches 54; Conservative 17; Mismatches 95; Indels 10; Gaps 5;
QY 27 RRHEQVEQYDCGRDPRDPYPYGEARPE----PRVDSRRRAARQSGPHETITLVG 82
DB 456 KQESKQPKQSPKDESPKPEQPKPEQPKPEQPKPEQPKPEQPKPEQPKPEQPKPEQ 515
QY 83 AVTSLQBLAHMARATHAPYGPYPVGVHHPHADTETPAQPPRYPAKAVYL--PPPHIA 140
DB 516 PVGNRRSPPPKVEDTRVP-EPQPM-PSPSPSPISYSPPPPVHSPSPSPSPSPSPSPSP 573
QY 141 PPGPLSGAVPPSPYPVAVTPGAPPLHQSPAHAHPPPPPGTTPPAASLROP 196
DB 574 SPSPSPV--ASPPSP 627

RESULT 14
T09965
extensin CYC17 precursor - Madagascarc periwinkle
C:Species: Catharanthus roseus (Madagascarc periwinkle)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: T09965
R.Ito, M.; Kodama, H.; Komamine, A.; Watanabe, A.
Plant Mol. Biol. 36, 343-351, 1998
A:Title: Expression of extensin genes is dependent on the stage of the cell cycle and ce
A:Reference number: Z16907; MUID:98145469; PMID:948475
A:Accession: T09965
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-217 <ITO>
A:Cross-references: UNIPROT:Q39600; EMBL:D86854; NID:g1486264; PIDN:BAAL3176.1; PID:g148
C:Genetics:
A:Function:
A:Description: structural component of the cell wall
C:Superfamily: proline-rich protein 3
C:Keywords: cell wall; glycoprotein; hydroxyproline

Query Match 15.5%; Score 191.5; DB 2; Length 217;
Best Local Similarity 39.7%; Pred. No. 4.2e-05;
Matches 52; Conservative 14; Mismatches 50; Indels 15; Gaps 7;
QY 78 TALVGAVTSLOQELAHMARATHAPYGPYPVGVHHPHADTETPAQPPRYPAKAVYL 135
DB 6 TALVIALVAL----CLPSQTTADYKYSPPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSP 60
QY 136 PP-HTAPGPPPLSGAVPPSPYPV--AVTPGAPPLHQ-PSPAHAHPPPPPP--GTPPP 188
DB 61 PTHKSP 119
QY 189 PAASLPQPEAP 199
DB 120 VYKSPSPSPKNP 130

RESULT 15
S57447
HPBR11-7 protein - human
N:Alternate names: HPBR11-4 protein
C:Species: Homo sapiens (man)
C:Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 16-Aug-2004
C:Accession: S57447; S57489
R:Flerschhauer, K.L.
submitted to the EMBL Data Library, June 1992
A:Reference number: S57447
A:Accession: S57447
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-551 <FILE>
A:Cross-references: UNIPROT:Q16630; EMBL:X67336; NID:g871300; PIDN:CAA47751.1; PID:g8713
A:Accession: S57489
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-551 <FL2>
A:Cross-references: EMBL:X67337; NID:g871298; PIDN:CAA47752.1; PID:g871299
C:Genetics:
A:Introns: 231/3
C:Superfamily: ribonucleoprotein repeat homology
F:82-151/Domain: ribonucleoprotein repeat homology <RRM4>

Query Match 15.4%; Score 190.5; DB 2; Length 551;
Best Local Similarity 36.0%; Pred. No. 0.00011;
Matches 49; Conservative 2; Mismatches 48; Indels 37; Gaps 5;
QY 104 PYPPVGVVHHPHADTETPAQPPRYPAKAVYLPPPHIAPP-----GPPPL 146
DB 237 PRPLGP-----PGPPGPPPPPGQVLPPLAGFPNNGDRPPPPVLPFGQFGQPP 288
QY 147 SGAVPPSPYPVAVTPGAPPLHQSPAHAHPPPP-----PPGTPPPPAASLPQPEAPG 200
DB 289 LGPLPPGPPPPV--PGYGPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSPSP 345
QY 201 AEAGALVNASSAAHVN 216
DB 346 PPPGA---PPPAHVN 358

Search completed: July 27, 2005, 12:22:24
Job time : 42 secs

This page blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 27, 2005, 12:06:17 ; Search time 44 Seconds
(without alignments)
380.032 Million cell updates/sec

Title: US-10-623-429-9_COPY_404_627
Perfect score: 1237
Sequence: 1 AIAADRQAGGLPAAAGDHGI.....ALVNASSAAHVNDTARAAD 224

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues
Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 670.5 | 54.2 | 635 | 4 | US-08-176-320-2 |
| 2 | 660.5 | 53.4 | 635 | 1 | Sequence 2, Appli |
| 3 | 190.5 | 15.4 | 553 | 4 | Sequence 7961, Ap |
| 4 | 190 | 15.4 | 324 | 4 | Sequence 7664, Ap |
| 5 | 189.5 | 15.3 | 498 | 4 | Sequence 7108, Ap |
| 6 | 184.5 | 14.9 | 559 | 4 | Sequence 2, Appli |
| 7 | 184.5 | 14.9 | 567 | 4 | Sequence 10952, A |
| 8 | 184 | 14.9 | 297 | 2 | Sequence 6, Appli |
| 9 | 184 | 14.9 | 297 | 3 | Sequence 2904, Ap |
| 10 | 179 | 14.5 | 511 | 4 | Sequence 24873, A |
| 11 | 178.5 | 14.4 | 142 | 4 | Sequence 235, App |
| 12 | 178 | 14.4 | 104 | 4 | Sequence 278, App |
| 13 | 178 | 14.4 | 707 | 4 | Sequence 993, App |
| 14 | 178 | 14.4 | 707 | 4 | Sequence 10120, A |
| 15 | 178 | 14.4 | 735 | 4 | Sequence 9978, Ap |
| 16 | 177.5 | 14.3 | 581 | 4 | Sequence 21050, A |
| 17 | 177 | 14.3 | 214 | 1 | Sequence 19531, A |
| 18 | 177 | 14.3 | 271 | 4 | Sequence 11282, A |
| 19 | 177 | 14.3 | 971 | 4 | Sequence 9, Appli |
| 20 | 176.5 | 14.3 | 1274 | 3 | Sequence 42632, A |
| 21 | 175.5 | 14.2 | 506 | 4 | Sequence 2, Appli |
| 22 | 175.5 | 14.2 | 684 | 4 | Sequence 24, Appli |
| 23 | 175 | 14.1 | 288 | 4 | Sequence 2, Appli |
| 24 | 175 | 14.1 | 503 | 4 | Sequence 2, Appli |
| 25 | 175 | 14.1 | 507 | 4 | Sequence 2, Appli |
| 26 | 173.5 | 14.0 | 1248 | 2 | Sequence 2, Appli |
| 27 | 173.5 | 14.0 | 1248 | 3 | Sequence 2, Appli |

ALIGNMENTS

RESULT 1
US-08-176-320-2
; Sequence 2, Application US/08176320
; Patent No. 6410704
; GENERAL INFORMATION:
; APPLICANT: Roizman, Bernard
; APPLICANT: Liu, Fenyong
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITLE OF INVENTION: PREPARATION AND USE OF A HERPES PROTEASE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Alice O. Martin
; STREET: 321 No. 6410704th Clark Street, Suite 800
; CITY: Chicago
; STATE: ILL
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/176,320
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/705,814
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooley, Ronald B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)744-0090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 635 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-176-320-2

Query Match 54.2%; Score 670.5; DB 4; Length 635;
Best Local Similarity 63.4%; Pred. No. 5.1e-44;
Matches 144; Conservative 12; Mismatches 64; Indels 7; Gaps 4;
QY 1 AIAADRQAGGLPAAAGDHGIRGSAKRHRHEVQPYDCGRDEPDRDFPYPYGEARPEPRP 60
DB 403 AIAADRQAGGQP-AAAGDPGVGSGRRRYEAGPSYSCDDQDFDADYPYPYGEARPG 461
QY 61 VDSRRRAARQASGPHETITATVAVTSLQOELAHMRARTHAPYGPVPFVGVPHPHADTE- 119

Sequence 4, Appli
Sequence 1, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 43, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 52, Appli
Sequence 4, Appli
Sequence 53, Appli
Sequence 3, Appli
Sequence 13993, A
Sequence 9746, Ap
Sequence 1338, Ap
Sequence 41, Appli
Sequence 47, Appli
Sequence 2, Appli
Sequence 19, Appli

| | | | |
|--|-----|---|-------------|
| Db | 462 | VDSRRRAARHSPTNETITATLMGAVTSLQOELAHMRARTSAPYGMTTPVAHYRPQVGEPEP | 521 |
| Qy | 120 | TPAQPPRYPKAVYLPPIHAPPGLSGA--VPPPSYPPVAVTPCGAPPLHQPSPAHAH | 177 |
| Db | 522 | TTTHPALCPPEAVYRPPPHSAPYGPQGPASHPTTPPYAPACPGPPPPP---- | PCPSTQT 578 |
| Qy | 178 | PPPPPPGPTPPPAASLQPEAPGABAGALVNASSAAHVNVDTRAAD | 224 |
| Db | 579 | RAPLPTFAFPFPAATGSGQPEASNAEAGALVNASSAAHVDVDTARAAD | 625 |
| RESULT 2 | | | |
| US-07-832-855-2 | | | |
| ; Sequence 2, Application US/07832855 | | | |
| ; Patent No. 5478727 | | | |
| ; GENERAL INFORMATION: | | | |
| ; APPLICANT: Roizman, Bernard | | | |
| ; APPLICANT: Liu, Fenyong | | | |
| ; TITLE OF INVENTION: Methods and Compositions of a | | | |
| ; TITLE OF INVENTION: Preparation and Use of A Herpes Protease | | | |
| ; NUMBER OF SEQUENCES: 15 | | | |
| ; CORRESPONDENCE ADDRESS: | | | |
| ; ADDRESSEE: ARNOLD, WHITE & DURKEE | | | |
| ; STREET: 321 No. 5478727th Clark Street, Suite 800 | | | |
| ; CITY: Chicago | | | |
| ; STATE: Illinois | | | |
| ; COUNTRY: USA | | | |
| ; ZIP: 60610 | | | |
| ; COMPUTER READABLE FORM: | | | |
| ; MEDIUM TYPE: Floppy disk | | | |
| ; COMPUTER: IBM PC compatible | | | |
| ; OPERATING SYSTEM: PC-DOS/MS-DOS | | | |
| ; SOFTWARE: PatentIn Release #1.0, Version #1.25 | | | |
| ; CURRENT APPLICATION DATA: US/07/832,855 | | | |
| ; APPLICATION NUMBER: US/07/832,855 | | | |
| ; FILING DATE: 19920207 | | | |
| ; CLASSIFICATION: 435 | | | |
| ; ATTORNEY/AGENT INFORMATION: | | | |
| ; NAME: Cooley, Ronald B. | | | |
| ; REGISTRATION NUMBER: 27,187 | | | |
| ; REFERENCE/DOCKET NUMBER: ARCD045 | | | |
| ; TELECOMMUNICATION INFORMATION: | | | |
| ; TELEPHONE: (312) 744-0090 | | | |
| ; TELEFAX: (312) 245-4961 | | | |
| ; INFORMATION FOR SEQ ID NO: 2: | | | |
| ; SEQUENCE CHARACTERISTICS: | | | |
| ; LENGTH: 635 amino acids | | | |
| ; TYPE: AMINO ACID | | | |
| ; TOPOLOGY: linear | | | |
| ; MOLECULE TYPE: protein | | | |
| US-07-832-855-2 | | | |
| Query Match 53.4%; Score 660.5; DB 1; Length 635; | | | |
| Best Local Similarity 62.6%; Pred. No. 3e-43; | | | |
| Matches 142; Conservative 12; Mismatches 66; Indels 7; Gaps 4 | | | |
| Qy | 1 | AIAADROAGGLPAAAGDHGICGSAXRRHVEQPEYDCGRDEPDRDFYYGGEARPERP | 60 |
| Db | 403 | AIAADROAGGQF--AAGDPGVGSGKRRRYEAGPSSEYCDDEPDADYPYYPGEARGAPRG | 461 |
| Qy | 61 | VDSRRARQASGPHETITATLVGAVTSLQOELAHMRARTHAPVGRYPYPVGVHHPHADTE- | 119 |
| Db | 462 | VDSRRARHSPTNETITATLMGAVTSLQOELAHMRARTSAPYGMTTPVAHYRPQVGEPEP | 521 |
| Qy | 120 | TPAQPPRYPKAVYLPPIHAPPGLSGA--VPPPSYPPVAVTPCGAPPLHQPSPAHAH | 177 |
| Db | 522 | TTTHPALCPPEAVYRPPPHSAPYGPQGPASHPTTPPYAPACPGPPPPP---- | PCPSTQT 578 |
| Qy | 178 | PPPPPPGPTPPPAASLQPEAPGABAGALVNASSAAHVNVDTRAAD | 224 |
| Db | 579 | RAPLPTFAFPFPPPTGSGQPEASNAEAGALVNASSAAHVDVDTARAAD | 625 |

Db 130 APSGPPGPPQLPPAPGVPAPVHP-----PASGVHPAPGVPAPGVPAPGVH 183
Qy 151 PPPS--YPPVAVTGPAPPLHQPSPAHHP-----PPPGPTPPPAASLPQPEAPGAE 203
Db 184 PPTSGVHPAPGVPAPGVPAPG--VHPAPGVPAPGVPAPGVPAPG--HPQAPGVHP 241
Qy 204 GA 205
Db 242 AA 243

RESULT 5
US-09-949-016-7108
; Sequence 7108, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7108
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7108

Query Match 15.3%; Score 189.5; DB 4; Length 498;
Best Local Similarity 32.1%; Pred. No. 4.3e-07;
Matches 54; Conservative 12; Mismatches 45; Indels 57; Gaps 9;

Qy 43 PDRDFYYGEPPEPRPVDSSRAARQASGPHETITLVGAVTSLQQLAHMRARTHAPY 102
Db 270 PPAEFY-----PVDNRGSLA-GPKRSW-----SPSHPP- 301

Qy 103 GPYPVGVYHHPADTETPAQPRYPKAVVLPPIHAPPGPLSGAVPPPSYPPV---- 158
Db 302 -PAPPLG-----SPGPG-----KPGFAPPAPPPPPPMIGIPPP--PPVGFGS 343

Qy 159 -AVTPGAPPLHQPSPAHHPPPPPGPT-----PPPAASLPQPEAP 199
Db 344 PGTTPPPSPFPHPHDFAAATPPPPPPPAADYPTLPPPLSQPTGGAP 391

RESULT 6
US-10-116-370-2
; Sequence 2, Application US/10116370
; Patent No. 6664068
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: PABLO, A POLYPEPTIDE THAT INTERACTS WITH BCL-XL, AND
; TITLE OF INVENTION: USES RELATED THERETO
; FILE REFERENCE: AM100012-D2
; CURRENT APPLICATION NUMBER: US/10/116,370
; CURRENT FILING DATE: 2002-04-04
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 559
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-116-370-2

Query Match 14.9%; Score 184.5; DB 4; Length 559;
Best Local Similarity 31.5%; Pred. No. 1.2e-06;
Matches 63; Conservative 13; Mismatches 79; Indels 45; Gaps 9;

Qy 55 RP-EPRPVDSSRAARQASGPHETITLVGAVTSLQQLAHMRARTHAPYGPYPVGVYH 113
Db 274 RPHEPPPPPMHMGAGDAKPIPTCISATGLIENRQSPA--TGRTPVFPVSTPPPPPL 331

Qy 114 PHADTETPAQPRYPKAVVLPPIHAPPGPP-----LSGAVPPPSYP-----PVAVTGP 164
Db 332 PSALSTSSLR-----ASMTSTPPPPVPPPPPPATLQAPAVPPPPAPLQIAPGVLPAP 386

Qy 165 ---APPLHQPSPAH-----PPPPPGTTPPPAASLPQPEAPG 200
Db 387 PPIAPPLVQSPFPVARAAPVCETVPVHPLPQGEVQGLPPPPPPPLPPPGI---RPSSP- 442

Qy 201 AEAGALVNASSAAHVNVDTA 220
Db 443 VVTVALAHPPSGLHPTPSTA 462

RESULT 7

US-09-949-016-10952
; Sequence 10952, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10952
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10952

Query Match 14.9%; Score 184.5; DB 4; Length 567;
Best Local Similarity 31.5%; Pred. No. 1.2e-06;
Matches 63; Conservative 13; Mismatches 79; Indels 45; Gaps 9;

Qy 55 RP-EPRPVDSSRAARQASGPHETITLVGAVTSLQQLAHMRARTHAPYGPYPVGVYH 113
Db 282 RPHEPPPPPMHMGAGDAKPIPTCISATGLIENRQSPA--TGRTPVFPVSTPPPPPL 339

Qy 114 PHADTETPAQPRYPKAVVLPPIHAPPGPP-----LSGAVPPPSYP-----PVAVTGP 164
Db 340 PSALSTSSLR-----ASMTSTPPPPVPPPPPPATLQAPAVPPPPAPLQIAPGVLPAP 394

Qy 165 ---APPLHQPSPAH-----PPPPPGTTPPPAASLPQPEAPG 200
Db 395 PPIAPPLVQSPFPVARAAPVCETVPVHPLPQGEVQGLPPPPPPPLPPPGI---RPSSP- 450

Qy 201 AEAGALVNASSAAHVNVDTA 220
Db 451 VVTVALAHPPSGLHPTPSTA 470

RESULT 8

US-08-580-545B-6
; Sequence 6, Application US/08580545B
; Patent No. 5932713
; GENERAL INFORMATION:
; APPLICANT: Yoshinisa, Kasukabe

```

? ZIP: 02354
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: CD-ROM ISO9660
? COMPUTER: <Unknown>
? OPERATING SYSTEM: <Unknown>
? SOFTWARE: <Unknown>
? CURRENT APPLICATION DATA:
?     APPLICATION NUMBER: US/09/107,433
?     FILING DATE: 30-Jun-1998
? PRIOR APPLICATION DATA:
?     APPLICATION NUMBER: 60/ 085131
?     FILING DATE: May 12, 1998
?     APPLICATION NUMBER: 60/051553
?     FILING DATE: July 2, 1997
? ATTORNEY/AGENT INFORMATION:
? NAME: Arianiello, Pamela Deneke
? REGISTRATION NUMBER: 40,489
? REFERENCE/DOCKET NUMBER: GTC-011
? TELECOMMUNICATION INFORMATION:
?     TELEPHONE: (781)893-5007
?     TELEFAX: (781)893-8277
? INFORMATION FOR SEQ ID NO: 2904:
? SEQUENCE CHARACTERISTICS:
?     LENGTH: 511 amino acids

```

[illegible]

```

; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratSeqFormatter Version 0.9
; SEQ ID NO 993
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)..(0)
; OTHER INFORMATION: Polypeptide Accession Number P23246
US-09-538-092-993

Query Match      14.4%; Score 178; DB 4; Length 707;
Best Local Similarity 39.7%; Pred. No. 4.8e-06;
Matches 46; Conservative 6; Mismatches 40; Indels 24; Gaps 6;

QY 103 GPYPVGVYHHADTETPAQPRYPYPAKAVYLPHPHIAPPGP-PLSGAVPPP-----SYP 156
Db 55 GKPEPIPP-PPHQQQQP--PPQQPPP--QQPPPHQPPHPHQHQPPPPQDSSKP 109
QY 157 PVAVTGPAPPLHQPSPAHAHPPP-----PPPGTTPPPAASLPQPEAP 199
Db 110 VVAGGPGAPGVGSAPPASSAPPATPTTSGAPPGSGGPTTTPPPAVTSAPPGAP 165

RESULT 15
US-09-949-016-10120
; Sequence 10120, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10120
; LENGTH: 735
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10120

Query Match      14.4%; Score 178; DB 4; Length 735;
Best Local Similarity 39.7%; Pred. No. 5e-06;
Matches 46; Conservative 6; Mismatches 40; Indels 24; Gaps 6;

QY 103 GPYPVGVYHHADTETPAQPRYPYPAKAVYLPHPHIAPPGP-PLSGAVPPP-----SYP 156
Db 83 GKPEPIPP-PPHQQQQP--PPQQPPP--QQPPPHQPPHPHQHQPPPPQDSSKP 137
QY 157 PVAVTGPAPPLHQPSPAHAHPPP-----PPPGTTPPPAASLPQPEAP 199
Db 138 VVAGGPGAPGVGSAPPASSAPPATPTTSGAPPGSGGPTTTPPPAVTSAPPGAP 193
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 27, 2005, 12:21:48 ; Search time 155 Seconds
(without alignments)
562.157 Million cell updates/sec

Title: US-10-623-429-9_COPY_404_627
Perfect score: 1237
Sequence: 1 AIAADRQAGGLPAAAGDHGI.....ALVNASSAAHVNVDARAAD 224

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1741741 seqs, 388992284 residues
Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| *Result No. | Score | Query Match | Length | ID | Description |
|-------------|-------|-------------|--------|----|----------------------|
| 1 | 1237 | 100.0 | 637 | 15 | US-10-623-429-9 |
| 2 | 670.5 | 54.2 | 635 | 14 | US-10-214-932-86 |
| 3 | 222 | 17.9 | 275 | 16 | US-10-425-115-315706 |
| 4 | 221.5 | 17.9 | 376 | 16 | US-10-767-701-42767 |
| 5 | 219.5 | 17.7 | 342 | 16 | US-10-437-963-112806 |
| 6 | 218.5 | 17.7 | 241 | 15 | US-10-424-599-224242 |
| 7 | 217 | 17.5 | 206 | 15 | US-10-424-599-224221 |
| 8 | 215.5 | 17.4 | 187 | 16 | US-10-425-115-352789 |
| 9 | 214 | 17.3 | 149 | 16 | US-10-425-115-252326 |
| 10 | 213.5 | 17.3 | 204 | 15 | US-10-424-599-221495 |
| 11 | 213.5 | 17.3 | 298 | 16 | US-10-437-963-147019 |

| | | | | | | |
|----|-------|------|-----|----|----------------------|-------------------|
| 12 | 213.5 | 17.3 | 639 | 15 | US-10-369-493-3962 | Sequence 3962, Ap |
| 13 | 213 | 17.2 | 147 | 15 | US-10-424-599-154677 | Sequence 154677, |
| 14 | 213 | 17.2 | 178 | 15 | US-10-424-599-264218 | Sequence 264218, |
| 15 | 213 | 17.2 | 223 | 16 | US-10-425-115-230534 | Sequence 230534, |
| 16 | 212 | 17.1 | 140 | 15 | US-10-424-599-276630 | Sequence 276630, |
| 17 | 211.5 | 17.1 | 296 | 15 | US-10-424-599-224246 | Sequence 224246, |
| 18 | 211 | 17.1 | 107 | 15 | US-10-424-599-234553 | Sequence 234553, |
| 19 | 211 | 17.1 | 329 | 17 | US-10-626-832-41 | Sequence 41, Appl |
| 20 | 211 | 17.1 | 497 | 16 | US-10-437-963-122257 | Sequence 122257, |
| 21 | 211 | 17.1 | 646 | 17 | US-10-626-832-42 | Sequence 42, Appl |
| 22 | 210 | 17.0 | 149 | 15 | US-10-424-599-278484 | Sequence 278484, |
| 23 | 210 | 17.0 | 273 | 16 | US-10-425-115-330708 | Sequence 330708, |
| 24 | 210 | 17.0 | 409 | 16 | US-10-437-963-140753 | Sequence 140753, |
| 25 | 209 | 16.9 | 183 | 16 | US-10-425-115-238672 | Sequence 238672, |
| 26 | 209 | 16.9 | 327 | 16 | US-10-425-115-276286 | Sequence 276286, |
| 27 | 208.5 | 16.9 | 187 | 16 | US-10-425-115-300973 | Sequence 300973, |
| 28 | 208.5 | 16.9 | 204 | 16 | US-10-437-963-119585 | Sequence 119585, |
| 29 | 208.5 | 16.9 | 235 | 16 | US-10-437-963-171176 | Sequence 171176, |
| 30 | 208 | 16.8 | 165 | 16 | US-10-767-701-35865 | Sequence 35865, A |
| 31 | 208 | 16.8 | 280 | 16 | US-10-425-115-231956 | Sequence 231956, |
| 32 | 207.5 | 16.8 | 236 | 16 | US-10-425-115-318599 | Sequence 318599, |
| 33 | 207 | 16.7 | 263 | 16 | US-10-437-963-116465 | Sequence 116465, |
| 34 | 206.5 | 16.7 | 180 | 16 | US-10-425-115-229737 | Sequence 229737, |
| 35 | 206.5 | 16.7 | 431 | 16 | US-10-437-963-204963 | Sequence 204963, |
| 36 | 206 | 16.7 | 189 | 15 | US-10-424-599-157515 | Sequence 157515, |
| 37 | 206 | 16.7 | 229 | 15 | US-10-424-599-207316 | Sequence 207316, |
| 38 | 205 | 16.6 | 252 | 16 | US-10-437-963-151853 | Sequence 151853, |
| 39 | 205 | 16.6 | 299 | 16 | US-10-437-963-134054 | Sequence 134054, |
| 40 | 204.5 | 16.5 | 133 | 16 | US-10-425-115-229322 | Sequence 229322, |
| 41 | 204.5 | 16.5 | 400 | 16 | US-10-425-115-278048 | Sequence 278048, |
| 42 | 204 | 16.5 | 125 | 16 | US-10-425-115-278144 | Sequence 278144, |
| 43 | 204 | 16.5 | 178 | 16 | US-10-425-115-321259 | Sequence 321259, |
| 44 | 204 | 16.5 | 208 | 16 | US-10-437-963-103915 | Sequence 103915, |
| 45 | 204 | 16.5 | 267 | 16 | US-10-425-115-238339 | Sequence 238339, |

ALIGNMENTS

RESULT 1
US-10-623-429-9
; Sequence 9, Application US/10623429
; Publication No. US20040072152A1
; GENERAL INFORMATION:
; APPLICANT: ZHI LIU
; APPLICANT: LAWRENCE COREY
; TITLE OF INVENTION: RAPID, EFFICIENT PURIFICATION OF
; TITLE OF INVENTION: HSV-SPECIFIC T-LYMPHOCYTES AND HSV ANTIGENS IDENTIFIED VIA
; FILE REFERENCE: 30967.11USU1
; CURRENT APPLICATION NUMBER: US/10/623,429
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 60/396,791
; PRIOR FILING DATE: 2002-07-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 637
; TYPE: PRT
; ORGANISM: Herpes Simplex Virus 2
US-10-623-429-9

| | | | | |
|-----------------------|-----------------|---|-----------|-------------|
| Query Match | 100.0% | Score 1237; | DB 15; | Length 637; |
| Best Local Similarity | 100.0% | Pred. No. 1.3e-72; | | |
| Matches 224; | Conservative 0; | Mismatches 0; | Indels 0; | Gaps 0; |
| QY | 1 | AIAADRQAGGLPAAAGDHGIRGSAKRREHVEQPSYDCGRDEPDRDFPYYPGEARPEPRP | 60 | |
| Db | 404 | AIAADRQAGGLPAAAGDHGIRGSAKRREHVEQPSYDCGRDEPDRDFPYYPGEARPEPRP | 463 | |
| QY | 61 | VDSRRARQAGSPHFTITALVCAVTSLOQLAHMARHAPYGPYPVPVGHPHADTET | 120 | |

Db 464 VDSRRARQASGPHETITLALVGAVTSLQQLAHMRARTHAPYGYPPVGVYHHPHADTET 523
Qy 121 PAOPPRYPKAVYLPPIPHIAPPGLSCGAVPPSPYPPVAVTGPAPPLHOPSPAHAPPP 180
Db 524 PAOPPRYPKAVYLPPIPHIAPPGLSCGAVPPSPYPPVAVTGPAPPLHOPSPAHAPPP 583
Qy 181 PPGPTPPPAASLPQPPAPGAEGALVNASAAHVNVDTARAAD 224
Db 584 PPGPTPPPAASLPQPPAPGAEGALVNASAAHVNVDTARAAD 627
RESULT 2
US-10-214-932-86
; Sequence 86, Application US/10214932
; Publication No. US20030100707A1
; GENERAL INFORMATION:
; APPLICANT: HWANG, Inwhan
; APPLICANT: KIM, Dae Heon
; APPLICANT: LEE, Yong Jik
; TITLE OF INVENTION: SYSTEM FOR DETECTING PROTEASE
; FILE REFERENCE: APB02/US
; CURRENT APPLICATION NUMBER: US/10/214,932
; CURRENT FILING DATE: 2002-08-08
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 86
; LENGTH: 635
; TYPE: PRT
; ORGANISM: Human herpesvirus 1
US-10-214-932-86
Query Match 54.2%; Score 670.5; DB 14; Length 635;
Best Local Similarity 63.4%; Pred. No. 9.3e-36;
Matches 144; Conservative 12; Mismatches 64; Indels 7; Gaps 4;
Qy 1 AIAADQAGGLPAAAGDHGIRGSAKRRRHEVEQPEYDCGRDEPDYPPYVGSARPEPRP 60
Db 403 AIAADQAGGQP--AAGDPGVGSGKRRRYEAGSESVCQDEPDADYPPYVGEARGPRG 461
Qy 61 VDSRRARQASGPHETITLALVGAVTSLQQLAHMRARTHAPYGYPPVGVYHHPHADTE- 119
Db 462 VDSRRARHSPTNETITLALMGAVTSLQQLAHMRARTSAPYGYMTPVAHYRPQVGEPEP 521
Qy 120 TPAQPRYPKAVYLPPIPHIAPPGLSGA--VPPSPYPVAVTGPAPPLHOPSPAHAH 177
Db 522 TTHPALCPPEAVYRPPPHSAPYGPQGPASHAPTTPYAPACPPGPPPP---PCPSTQT 578
Qy 178 PPPPPPGPTPPPAASLPQPPAPGAEGALVNASAAHVNVDTARAAD 224
Db 579 RAPLPTEPAPPPATGSPQPEASNAEAGALVNASAAHVNVDTARAAD 625
RESULT 3
US-10-425-115-315706
; Sequence 315706, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 315706
; LENGTH: 275
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure

; LOCATION: (1)..(275)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_50997C.1.pep
US-10-425-115-315706
Query Match 17.9%; Score 222; DB 16; Length 275;
Best Local Similarity 28.6%; Pred. No. 6.3e-07;
Matches 67; Conservative 10; Mismatches 83; Indels 74; Gaps 7;
Qy 1 AIAADQAGGLPAAAGDHGIRGSAKRRRHEVEQPEYDCGR-----D 41
Db 1 SLCFGRAGG---CGGRHGPPRRALPGDCGAQRRLRYIRRRRRFRGRAAGGLPRSQSPGD 57
Qy 42 EPDRD-----FPYVPGEARPEPRVDSERRARQASGPHETITLALVGAVTSLQOE 90
Db 58 EPPREKVPKTPYPSXTPHARSDTPPXPPD----- 87
Qy 91 LAHMRARTHA-PYGPVPPVGVYHHPHADTETPAQPRYPKAVYLPPIPHIAPPGLPLSGA 149
Db 88 -----HAPPPPPPLPPGAPXPFPFPFPFPFPFPFPFPFPFPFPFPFPFPFPFP 139
Qy 150 VPPSPYPVAVTGPAPPLHOPSPAHAPPPPPPGTTPPAAASLPQPEAFGAEA 203
Db 140 RPPD--PPPGPPPPAPXPFPFPFPFPFPFPFPFPFPFPFPFPFPFPFPFP 191
RESULT 4
US-10-767-701-42767
; Sequence 42767, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 42767
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C17099_1.pep
US-10-767-701-42767
Query Match 17.9%; Score 221.5; DB 16; Length 376;
Best Local Similarity 34.1%; Pred. No. 9.1e-07;
Matches 71; Conservative 4; Mismatches 54; Indels 79; Gaps 11;
Qy 4 ADRQAG-GLPAAAGDHGIRGSAKRRRHEVEQPEYDCGRDEPDYPPYVGEARPEPRPD 62
Db 16 APRPFGGLPASA----CRGPRRRGRCRCPD-----APPPRPPG 52
Qy 63 SRRAA--RQASGPHETITLALVGAVTSLQQLAHMRARTHAPYGYPP-----VGYPYHHPHA 116
Db 53 GPPAAGPRPAPGP-----PPCGFPFPFPAPRAAGFGGPG-- 84
Qy 117 DTETPAQPRYPKAVYLPPIPHIAPPGLSGAVPPSPYPPVAVTGPAPPLHOPSPAH 176
Db 85 -----PAPPPPPP-----PPPPAPPPPPP-----PPF--PPFAPPPPPPPPPGPPAD--- 124
Qy 177 HPPPPPPPGTTPPAAASLPQPEAFGAEG 204
Db 125 -PP 151
RESULT 5
US-10-437-963-112806
; Sequence 112806, Application US/10437963

Publication No. US2004012343A1
GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 112806
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(342)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_16656C.1.pap
US-10-437-963-112806

Query Match 17.7%; Score 219.5; DB 16; Length 342;
Best Local Similarity 28.9%; Pred. No. 1.1e-06;
Matches 70; Conservative 8; Mismatches 81; Indels 83; Gaps 10;
Qy 12 PARAGDHGIRGSAKRREHEVQPEYDCGRDPRDRFYYPGCEARPEPRPVDSSRAARQAS 71
Db 11 PHRAG----RGARSTDDPAAQPH-----DPPPHXPQPPPTHTPLPPAGAPTRH 60
Qy 72 GPHEITLVGAVTSLQOELAHMRARTHAPYGPYPVGYHH-----PHADTET--- 120
Db 61 TPQHHTTA-----PHKKKPTRPTXPPPPPPSHSPPPPXSLPHPPPTPTP 108
Qy 121 -----PAQPPRYPAKAVLPPPHIAPPGLSGAVPPSPYPVAVTPGAPPLH 169
Db 109 TTPHTTHPPPPHPPRNPKNPITPPPIITPPPPP-----PPSPPPP--HPPPPPPPPH 161
Qy 170 QPSP--AAHAPPPPPP-----GPTPPPA-----SLPQPE 197
Db 162 SPTPLTPRRQPPLPLSHGNTNPLSLGTPTPPPPPXPRSKRPPAGQINPPIDSLRPP 221
Qy 198 AP 199
Db 222 PP 223

RESULT 6
US-10-424-599-163337
; Sequence 163337, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 163337
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:

; NAME/KEY: unsure
; LOCATION: (1)..(241)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_118511C.1.pap
US-10-424-599-163337

Query Match 17.7%; Score 218.5; DB 15; Length 241;
Best Local Similarity 43.1%; Pred. No. 9.4e-07;
Matches 44; Conservative 4; Mismatches 53; Indels 1; Gaps 1;
Qy 99 HAPYGPYPVGPY-HHPHADTETPAQPPRYPAKAVLPPPHIAPPGLSGAVPPSPYP 157
Db 37 HPPPPXPPPHPHSHHDPDPSPTAIPDDPIPKPHPPPPPPXPLPLPPPPPPPPPPPP 96
Qy 158 VAVTGPAPPLHQPSPAHAHPPPPPGTPTPPPAASLQPEAP 199
Db 97 PPP 138

RESULT 7
US-10-424-599-224421
; Sequence 224421, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 224421
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(206)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_44681C.1.pap
US-10-424-599-224421

Query Match 17.5%; Score 217; DB 15; Length 206;
Best Local Similarity 39.6%; Pred. No. 1e-06;
Matches 61; Conservative 5; Mismatches 68; Indels 20; Gaps 7;
Qy 50 YPGEARPEPRPVDSSRAARQASGPHETITLVGAVTSLQOELAHMRARTHAPYGPYPVG 109
Db 59 YHGPPRC-PR-ADRPHTTRPTSPHHTPPA-----AHPPPLRPMRTRLPPLPPPPPTRA 110
Qy 110 PYHHPHADTETPAQPPRYPAKAVLPPPHIAPPGLSGAVPPSPYPVAVTPGAPPL 168
Db 111 P---PPPTPAPCGPPXPXHPPLCPPPPPPSASPLPPPPPPPPXPPPPPPPLHISPLTPPP 167
Qy 169 HQPSAH-----AHPPPPPGTPT---PPAASLP 194
Db 168 TSPPPPHYTPSPXPPPPPPPPPTTPPLPLPPAPLP 201

RESULT 8
US-10-425-115-352789
; Sequence 352789, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei

```
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 352789
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(187)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_84911C.1.pep
US-10-425-115-352789

Query Match      17.4%; Score 215.5; DB 16; Length 187;
Best Local Similarity 36.8%; Pred. No. 1.2e-06;
Matches 57; Conservative 3; Mismatches 66; Indels 29; Gaps 6;

QY 48 PYPFGARPRPRVDSRRARQASGPHETITALTALVGAVTSLQQLAHMRARTHAPYG---P 104
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 10 PLTPAPAPPPPPAP---PLTPATAPHT-----RPLPHSR-----PIGTTPP 50

QY 105 YPPVGPVHHPHADTETPAQPRYPKAVYLPDPHIAPPGPPSLGAVPPSPYPVAVTTPG 164
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 51 PPPTPRLRPAPPPXPTPTPPPLFSPPPPPPPPPPPPPPPS---PPPPPPPPPPPPHP 107

QY 165 APPLHPSPAHAHPPPPPPPPGPTTPPAASLPQPEAP 199
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 108 PPPLPPPPP-----PPPPPPPPPPPPPPPPPPPPPP 138

RESULT 9
US-10-425-115-252326
; Sequence 252326, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 252326
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(149)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_161704C.1.pep
US-10-425-115-252326

Query Match      17.3%; Score 214; DB 16; Length 149;
Best Local Similarity 36.4%; Pred. No. 1.2e-06;
Matches 52; Conservative 4; Mismatches 63; Indels 24; Gaps 5;

QY 58 PRVDSRRARQASGPHETITALTALVGAVTSLQQLAHMRARTHAPYGY--PPVGPVHHPH 115
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 25 PPPPD-----HQNKPHNHPT-----PHSKTQTPTPPPHPPPPSTTHHHR 66

QY 116 ADTETPAQPRYPKAVYLPDPHIAPPGP--PLSGAVPPSPYPVAVTTPGAPPLHQPS 173
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 67 NPPIPTPPXPPPPPPXPPPHAPPPPTTTPPNHTPPPPXPPPHHTPHPPPTTTPPP 126
```

```
QY 174 AHAHPPP--PPPGTTPPPAASLP 194
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 127 PHPHQTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPTPT 149

RESULT 10
US-10-424-599-221495
; Sequence 221495, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 221495
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(204)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_42039C.1.pep
US-10-424-599-221495

Query Match      17.3%; Score 213.5; DB 15; Length 204;
Best Local Similarity 44.6%; Pred. No. 1.7e-06;
Matches 50; Conservative 0; Mismatches 49; Indels 13; Gaps 4;

QY 101 PYGYPVPVGVYHHPH-----ADTETPAQPRYPKAVYLPDPHIA-PPGPPPLSGA 149
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 13 PSGFAPPPGPPPPXPPSPGPPPPGXPLPPPPGPPPLGAPLPGLPPPPPPGPPPPPP 72

QY 150 VPPSPYPPVAVTTPGAPPLHQPSPAHAHPP--PPPGTTPPPAASLPQPEAPG 200
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 73 TTPPGPPPPPLGAPLPGLGSPPPGAPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 123

RESULT 11
US-10-437-963-147019
; Sequence 147019, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 147019
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(298)
; OTHER INFORMATION: unsure at all Xaa locations
```

FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_47588C.1.pep
US-10-437-963-147019

Query Match 17.3%; Score 213.5; DB 15; Length 298;
Best Local Similarity 30.5%; Pred. No. 2.4e-06;
Matches 61; Conservative 5; Mismatches 91; Indels 43; Gaps 5;
QY 6 ROAGGLPAAAGDHGIRGSAKRREHEVQPEYD-CGRDEPRDRFP-----YYPGEARPEPR 59
DB 22 RSPGGGQDAGHGHPADPDRLDNAQPPSRDAASQTAPDTLPXKTPXHAFTXRRPPPP 81
QY 60 PVDSSRAARQASGPHETITLVGAVTSLQELAHMRATHAPYGPYPVGVYHHPHADTE 119
DB 82 P-----PPQP-----PPTPPPPPPPPPTPPPPPP----- 105
QY 120 TPAQPPRYPAKANVLPPLHATPGCPPLSGAVPPSYPPVATGCPAPLHQPSPAHAAHP 179
DB 106 -PP 164
QY 180 PPPPGTTPPPAASLPQPEAP 199
DB 165 PPP 184

RESULT 12
US-10-369-493-3962
Sequence 3962, Application US/10369493
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
PRIOR FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 3962
LENGTH: 639
TYPE: PRT
ORGANISM: Neurospora crassa
US-10-369-493-3962

Query Match 17.3%; Score 213.5; DB 15; Length 639;
Best Local Similarity 28.4%; Pred. No. 4.9e-06;
Matches 73; Conservative 19; Mismatches 102; Indels 63; Gaps 11;
QY 28 RHEVQPEYDCGR---DEPRDRFPYYPG---EARPEPRVDSRRRAARQASGP----- 73
DB 339 RFVAPPPADAGKPAHSDPPRHPTSPAGPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 398
QY 74 -----HETITLVGAVTSLQELAHMRATHAPYGPYPVGVYHHPHADTEPAQPPR 126
DB 399 VPPPPPPSSVPP 456
QY 127 YPAKAVILPPP-----HIAPGPPLSGAVPPSYPPVATGCPAPL---HOPSP----- 173
DB 457 PPLTSNAPPPPPPLPATQAPPPPLPATSPAPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 515
QY 174 -----AHAPPPPPPPG-----PTPPAASLPQPEAP-----GAEAGALVNASS 211
DB 516 PMPAPSGGAPPP 575
QY 212 AAHV-----NVTARAAD 224
DB 576 AGGIRALKKVDRSQIRD 592

RESULT 13
US-10-424-599-154677
Sequence 154677, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 154677
LENGTH: 147
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(147)
OTHER INFORMATION: unsure at all xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_110695C.1.pep
US-10-424-599-154677

Query Match 17.2%; Score 213; DB 15; Length 147;
Best Local Similarity 42.1%; Pred. No. 1.3e-06;
Matches 45; Conservative 3; Mismatches 47; Indels 12; Gaps 3;
QY 104 PYPPVGVYHHPHADTETP-----AOPPRYPKAVYLPPIHAPPGLSGAVPPPSYP 156
DB 1 PPTTTPPP 57
QY 157 PVATPGPAPLHQPSPAHAAHPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPPP 203
DB 58 PPTTTPPP 102

RESULT 14
US-10-424-599-264218
Sequence 264218, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 264218
LENGTH: 178
TYPE: PRT
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(178)
OTHER INFORMATION: unsure at all xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT3847_8060C.1.pep
US-10-424-599-264218

Query Match 17.2%; Score 213; DB 15; Length 178;
Best Local Similarity 45.0%; Pred. No. 1.6e-06;
Matches 45; Conservative 1; Mismatches 48; Indels 6; Gaps 2;
QY 101 PYGPPVGVYHHPHADTET-PAOPPRYPKAVYLPPIHAPPGLSGAVPPPSYP 159

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 27, 2005, 12:32:44 ; Search time 41 Seconds
(without alignments)
16.386 Million cell updates/sec

Title: US-10-623-429-9_COPY_475_483

Perfect score: 48

Sequence: 1 GPHETITAL 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA.*

1: /cgm2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgm2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgm2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgm2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgm2_6/ptodata/1/iaa/ECTUS_COMB.pep.*
6: /cgm2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|----------------------|
| 1 | 36 | 75.0 | 50 | 3 | US-09-346-860-9 |
| 2 | 36 | 75.0 | 50 | 4 | US-09-735-685-9 |
| 3 | 36 | 75.0 | 79 | 3 | US-08-905-223-493 |
| 4 | 35 | 72.9 | 58 | 4 | US-10-127-641-5 |
| 5 | 35 | 72.9 | 91 | 4 | US-09-248-796A-19847 |
| 6 | 35 | 72.9 | 748 | 2 | US-08-997-080-154 |
| 7 | 35 | 72.9 | 748 | 2 | US-08-997-362-154 |
| 8 | 35 | 72.9 | 748 | 3 | US-09-095-855-154 |
| 9 | 35 | 72.9 | 748 | 3 | US-09-324-542-154 |
| 10 | 35 | 72.9 | 748 | 4 | US-09-205-426-154 |
| 11 | 35 | 72.9 | 754 | 3 | US-09-005-180A-3 |
| 12 | 34 | 70.8 | 102 | 4 | US-09-513-999C-6366 |
| 13 | 34 | 70.8 | 154 | 4 | US-09-615-192A-311 |
| 14 | 34 | 70.8 | 300 | 4 | US-09-134-000C-5791 |
| 15 | 34 | 70.8 | 699 | 4 | US-09-252-991A-17077 |
| 16 | 34 | 70.8 | 717 | 4 | US-09-543-681A-5706 |
| 17 | 34 | 70.8 | 762 | 4 | US-09-107-532A-4275 |
| 18 | 34 | 70.8 | 2584 | 4 | US-08-936-135-4 |
| 19 | 34 | 70.8 | 2588 | 3 | US-08-936-135-2 |
| 20 | 33 | 68.8 | 81 | 4 | US-09-107-532A-7025 |
| 21 | 33 | 68.8 | 364 | 4 | US-09-252-991A-22552 |
| 22 | 33 | 68.8 | 401 | 4 | US-09-248-796A-19514 |
| 23 | 33 | 68.8 | 635 | 1 | US-07-832-855-2 |
| 24 | 33 | 68.8 | 635 | 4 | US-08-176-320-2 |
| 25 | 33 | 68.8 | 726 | 4 | US-09-489-039A-8750 |
| 26 | 33 | 68.8 | 1009 | 4 | US-09-762-724-10 |
| 27 | 33 | 68.8 | 1017 | 4 | US-09-762-724-12 |

| | | | | | | |
|-----|----|------|-------|---|----------------------|-------------------|
| 28 | 33 | 68.8 | 1023 | 4 | US-09-762-724-14 | Sequence 14, Appl |
| 29 | 33 | 68.8 | 1027 | 4 | US-09-762-724-8 | Sequence 8, Appl |
| 30 | 32 | 66.7 | 108 | 4 | US-09-513-999C-5317 | Sequence 5317, Ap |
| 31 | 32 | 66.7 | 277 | 3 | US-09-007-484-4 | Sequence 4, Appl |
| 32 | 32 | 66.7 | 277 | 3 | US-09-309-682-4 | Sequence 4, Appl |
| 33 | 32 | 66.7 | 305 | 3 | US-09-335-409-22 | Sequence 22, Appl |
| 34 | 32 | 66.7 | 305 | 3 | US-09-568-102-22 | Sequence 22, Appl |
| 35 | 32 | 66.7 | 305 | 3 | US-09-567-969-22 | Sequence 22, Appl |
| 36 | 32 | 66.7 | 305 | 3 | US-09-568-480-22 | Sequence 22, Appl |
| 37 | 32 | 66.7 | 305 | 3 | US-09-568-486-22 | Sequence 22, Appl |
| 38 | 32 | 66.7 | 305 | 3 | US-09-568-472-22 | Sequence 22, Appl |
| 39 | 32 | 66.7 | 305 | 3 | US-09-567-899-22 | Sequence 22, Appl |
| 40 | 32 | 66.7 | 307 | 4 | US-09-328-352-4994 | Sequence 4994, Ap |
| 41 | 32 | 66.7 | 315 | 4 | US-09-902-540-11852 | Sequence 11852, A |
| 42 | 32 | 66.7 | 383 | 4 | US-09-489-039A-12482 | Sequence 12482, A |
| 43 | 32 | 66.7 | 425 | 2 | US-08-986-963-2 | Sequence 2, Appl |
| 44 | 32 | 66.7 | 429 | 4 | US-09-583-110-4561 | Sequence 4561, Ap |
| 45 | 32 | 66.7 | 430 | 3 | US-09-007-484-2 | Sequence 2, Appl |
| 46 | 32 | 66.7 | 430 | 3 | US-09-309-682-2 | Sequence 2, Appl |
| 47 | 32 | 66.7 | 430 | 4 | US-09-107-433-2686 | Sequence 2686, Ap |
| 48 | 32 | 66.7 | 431 | 4 | US-09-540-236-2280 | Sequence 2280, Ap |
| 49 | 32 | 66.7 | 492 | 3 | US-09-413-814-72 | Sequence 72, Appl |
| 50 | 32 | 66.7 | 536 | 4 | US-09-328-352-7300 | Sequence 7300, Ap |
| 51 | 32 | 66.7 | 536 | 4 | US-09-653-274-10 | Sequence 10, Appl |
| 52 | 32 | 66.7 | 536 | 4 | US-10-461-791-10 | Sequence 10, Appl |
| 53 | 32 | 66.7 | 930 | 4 | US-08-254-594-6 | Sequence 6, Appl |
| 54 | 32 | 66.7 | 1385 | 2 | US-08-687-399-7 | Sequence 7, Appl |
| 55 | 32 | 66.7 | 2042 | 4 | US-09-489-039A-14053 | Sequence 14053, A |
| 56 | 31 | 64.6 | 82 | 4 | US-09-134-000C-5571 | Sequence 5571, Ap |
| 57 | 31 | 64.6 | 129 | 4 | US-09-270-767-32657 | Sequence 32657, A |
| 58 | 31 | 64.6 | 129 | 4 | US-09-270-767-47874 | Sequence 47874, A |
| 59 | 31 | 64.6 | 174 | 4 | US-09-496-118B-5 | Sequence 5, Appl |
| 60 | 31 | 64.6 | 262 | 4 | US-09-252-991A-25231 | Sequence 25231, A |
| 61 | 31 | 64.6 | 270 | 4 | US-09-270-767-37404 | Sequence 37404, A |
| 62 | 31 | 64.6 | 270 | 4 | US-09-270-767-52621 | Sequence 52621, A |
| 63 | 31 | 64.6 | 285 | 3 | US-09-286-529-1 | Sequence 1, Appl |
| 64 | 31 | 64.6 | 285 | 4 | US-09-589-287B-2 | Sequence 2, Appl |
| 65 | 31 | 64.6 | 285 | 4 | US-09-496-118B-1 | Sequence 1, Appl |
| 66 | 31 | 64.6 | 285 | 4 | US-09-565-423-2 | Sequence 2, Appl |
| 67 | 31 | 64.6 | 285 | 4 | US-09-879-919-23 | Sequence 23, Appl |
| 68 | 31 | 64.6 | 285 | 4 | US-09-588-947A-2 | Sequence 2, Appl |
| 69 | 31 | 64.6 | 285 | 4 | US-09-589-286A-2 | Sequence 2, Appl |
| 70 | 31 | 64.6 | 285 | 4 | US-09-005-874-2 | Sequence 2, Appl |
| 71 | 31 | 64.6 | 285 | 4 | US-09-255-794A-2 | Sequence 2, Appl |
| 72 | 31 | 64.6 | 285 | 4 | US-09-507-968D-2 | Sequence 2, Appl |
| 73 | 31 | 64.6 | 289 | 4 | US-09-949-016-8108 | Sequence 8108, Ap |
| 74 | 31 | 64.6 | 315 | 4 | US-09-248-796A-19855 | Sequence 19855, A |
| 75 | 31 | 64.6 | 328 | 3 | US-08-858-003-31 | Sequence 31, Appl |
| 76 | 31 | 64.6 | 328 | 3 | US-09-078-166-31 | Sequence 31, Appl |
| 77 | 31 | 64.6 | 328 | 3 | US-08-997-467-31 | Sequence 31, Appl |
| 78 | 31 | 64.6 | 364 | 4 | US-09-438-046-13 | Sequence 13, Appl |
| 79 | 31 | 64.6 | 417 | 4 | US-09-533-494A-2 | Sequence 2, Appl |
| 80 | 31 | 64.6 | 566 | 4 | US-09-514-245-21 | Sequence 21, Appl |
| 81 | 31 | 64.6 | 668 | 1 | US-08-530-950-13 | Sequence 13, Appl |
| 82 | 31 | 64.6 | 668 | 3 | US-09-149-879-13 | Sequence 13, Appl |
| 83 | 31 | 64.6 | 668 | 4 | US-09-057-009-13 | Sequence 13, Appl |
| 84 | 31 | 64.6 | 735 | 4 | US-09-252-991A-32240 | Sequence 32240, A |
| 85 | 31 | 64.6 | 772 | 4 | US-10-148-806-37 | Sequence 37, Appl |
| 86 | 31 | 64.6 | 1040 | 2 | US-08-254-989-2 | Sequence 2, Appl |
| 87 | 31 | 64.6 | 1302 | 4 | US-09-538-052-935 | Sequence 935, App |
| 88 | 31 | 64.6 | 1302 | 4 | US-09-902-540-14853 | Sequence 14853, A |
| 89 | 31 | 64.6 | 1700 | 4 | US-09-949-016-10503 | Sequence 10503, A |
| 90 | 31 | 64.6 | 1770 | 4 | US-09-902-540-10224 | Sequence 10224, A |
| 91 | 31 | 64.6 | 2594 | 3 | US-08-718-388-7 | Sequence 7, Appl |
| 92 | 31 | 64.6 | 5405 | 3 | US-08-718-388-9 | Sequence 9, Appl |
| 93 | 31 | 64.6 | 15281 | 2 | US-08-471-119A-2 | Sequence 2, Appl |
| 94 | 30 | 62.5 | 25 | 1 | US-07-792-259-3 | Sequence 3, Appl |
| 95 | 30 | 62.5 | 42 | 2 | US-08-441-871-82 | Sequence 82, Appl |
| 96 | 30 | 62.5 | 62 | 4 | US-09-107-532A-5561 | Sequence 5561, Ap |
| 97 | 30 | 62.5 | 71 | 4 | US-09-248-796A-21256 | Sequence 21256, A |
| 98 | 30 | 62.5 | 74 | 4 | US-09-248-796A-25684 | Sequence 25684, A |
| 99 | 30 | 62.5 | 158 | 2 | US-08-403-852D-29 | Sequence 29, Appl |
| 100 | 30 | 62.5 | 158 | 3 | US-08-510-646B-30 | Sequence 30, Appl |

| | | | | | | | | | | | | | |
|-----|----|------|------|---|----------------------|--------------------|-----|------|------|------|---|----------------------|-------------------|
| 101 | 30 | 62.5 | 158 | 3 | US-09-231-818-29 | Sequence 29, Appl | 174 | 29 | 60.4 | 395 | 4 | US-09-710-279-26 | Sequence 26, Appl |
| 102 | 30 | 62.5 | 158 | 4 | US-09-635-359B-29 | Sequence 29, Appl | 175 | 29 | 60.4 | 402 | 4 | US-09-252-991A-31080 | Sequence 31080, A |
| 103 | 30 | 62.5 | 179 | 4 | US-09-615-392A-289 | Sequence 289, Appl | 176 | 29 | 60.4 | 406 | 3 | US-09-134-001C-5330 | Sequence 5330, Ap |
| 104 | 30 | 62.5 | 202 | 4 | US-09-134-000C-3978 | Sequence 3978, Ap | 177 | 29 | 60.4 | 416 | 4 | US-09-134-000C-5375 | Sequence 5375, Ap |
| 105 | 30 | 62.5 | 221 | 4 | US-09-248-796A-16638 | Sequence 16638, A | 178 | 29 | 60.4 | 422 | 4 | US-09-252-991A-21999 | Sequence 21999, A |
| 106 | 30 | 62.5 | 223 | 4 | US-09-328-352-4358 | Sequence 4358, Ap | 179 | 29 | 60.4 | 426 | 4 | US-09-711-164-380 | Sequence 380, App |
| 107 | 30 | 62.5 | 264 | 4 | US-09-543-681A-6332 | Sequence 6332, Ap | 180 | 29 | 60.4 | 470 | 4 | US-09-270-767-61004 | Sequence 61004, A |
| 108 | 30 | 62.5 | 266 | 4 | US-09-134-000C-3456 | Sequence 3456, Ap | 181 | 29 | 60.4 | 485 | 4 | US-09-252-991A-27501 | Sequence 27501, A |
| 109 | 30 | 62.5 | 304 | 4 | US-09-543-681A-8200 | Sequence 8200, Ap | 182 | 29 | 60.4 | 513 | 4 | US-09-142-108C-42 | Sequence 42, Appl |
| 110 | 30 | 62.5 | 331 | 4 | US-09-902-540-10221 | Sequence 10221, A | 183 | 29 | 60.4 | 518 | 2 | US-08-836-620A-18 | Sequence 18, Appl |
| 111 | 30 | 62.5 | 339 | 4 | US-09-489-039A-12231 | Sequence 12231, A | 184 | 29 | 60.4 | 568 | 1 | US-07-803-622B-4 | Sequence 4, Appl |
| 112 | 30 | 62.5 | 343 | 2 | US-08-624-545-1 | Sequence 1, Appl | 185 | 29 | 60.4 | 582 | 3 | US-09-242-632A-2 | Sequence 2, Appl |
| 113 | 30 | 62.5 | 343 | 2 | US-09-235-736-1 | Sequence 1, Appl | 186 | 29 | 60.4 | 601 | 4 | US-09-270-767-45496 | Sequence 45496, A |
| 114 | 30 | 62.5 | 344 | 3 | US-09-024-532-4 | Sequence 4, Appl | 187 | 29 | 60.4 | 615 | 4 | US-09-198-452A-1037 | Sequence 1037, Ap |
| 115 | 30 | 62.5 | 344 | 4 | US-09-705-185-4 | Sequence 12, Appl | 188 | 29 | 60.4 | 668 | 4 | US-09-452-991A-22794 | Sequence 22794, A |
| 116 | 30 | 62.5 | 345 | 1 | US-07-792-259-12 | Sequence 12, Appl | 189 | 29 | 60.4 | 677 | 2 | US-08-522-269B-3 | Sequence 3, Appl |
| 117 | 30 | 62.5 | 363 | 1 | US-08-458-023B-6 | Sequence 6, Appl | 190 | 29 | 60.4 | 677 | 3 | US-09-294-923-3 | Sequence 3, Appl |
| 118 | 30 | 62.5 | 364 | 1 | US-07-792-259-17 | Sequence 17, Appl | 191 | 29 | 60.4 | 753 | 3 | US-09-276-400-2 | Sequence 2, Appl |
| 119 | 30 | 62.5 | 368 | 4 | US-09-134-000C-4478 | Sequence 4478, Ap | 192 | 29 | 60.4 | 753 | 3 | US-09-448-076-2 | Sequence 2, Appl |
| 120 | 30 | 62.5 | 384 | 4 | US-09-252-991A-26093 | Sequence 26093, A | 193 | 29 | 60.4 | 753 | 3 | US-09-702-572-2 | Sequence 2, Appl |
| 121 | 30 | 62.5 | 385 | 4 | US-09-252-991A-26432 | Sequence 26432, A | 194 | 29 | 60.4 | 768 | 4 | US-09-134-000C-6467 | Sequence 6467, Ap |
| 122 | 30 | 62.5 | 392 | 2 | US-08-387-942C-23 | Sequence 23, Appl | 195 | 29 | 60.4 | 777 | 4 | US-09-811-469-2 | Sequence 2, Appl |
| 123 | 30 | 62.5 | 435 | 2 | US-08-331-515A-2 | Sequence 2, Appl | 196 | 29 | 60.4 | 777 | 4 | US-10-370-659-2 | Sequence 2, Appl |
| 124 | 30 | 62.5 | 435 | 3 | US-09-168-406A-2 | Sequence 2, Appl | 197 | 29 | 60.4 | 885 | 4 | US-09-502-540-13431 | Sequence 13431, A |
| 125 | 30 | 62.5 | 446 | 4 | US-09-949-016-7571 | Sequence 7571, Ap | 198 | 29 | 60.4 | 929 | 4 | US-09-254-594-3 | Sequence 3, Appl |
| 126 | 30 | 62.5 | 480 | 4 | US-09-252-991A-20125 | Sequence 20125, A | 199 | 29 | 60.4 | 981 | 4 | US-09-991-258-13 | Sequence 13, Appl |
| 127 | 30 | 62.5 | 493 | 4 | US-09-583-110-2996 | Sequence 2996, Ap | 200 | 29 | 60.4 | 998 | 4 | US-09-198-452A-841 | Sequence 841, App |
| 128 | 30 | 62.5 | 495 | 4 | US-09-107-532A-6687 | Sequence 6687, Ap | 201 | 29 | 60.4 | 998 | 4 | US-09-438-185A-793 | Sequence 793, App |
| 129 | 30 | 62.5 | 499 | 4 | US-09-107-433-4478 | Sequence 4478, Ap | 202 | 29 | 60.4 | 1306 | 3 | US-08-999-774A-13 | Sequence 13, Appl |
| 130 | 30 | 62.5 | 502 | 4 | US-09-134-000C-6237 | Sequence 6237, Ap | 203 | 29 | 60.4 | 1317 | 4 | US-09-949-016-7588 | Sequence 7588, Ap |
| 131 | 30 | 62.5 | 502 | 4 | US-09-949-016-5991 | Sequence 5991, Ap | 204 | 29 | 60.4 | 1326 | 4 | US-09-688-188B-15 | Sequence 15, Appl |
| 132 | 30 | 62.5 | 513 | 4 | US-09-465-558-36 | Sequence 36, Appl | 205 | 29 | 60.4 | 1326 | 4 | US-09-291-417B-15 | Sequence 15, Appl |
| 133 | 30 | 62.5 | 553 | 2 | US-08-387-942C-2 | Sequence 2, Appl | 206 | 29 | 60.4 | 1805 | 4 | US-09-949-016-8246 | Sequence 8246, Ap |
| 134 | 30 | 62.5 | 649 | 4 | US-09-902-540-13928 | Sequence 13928, A | 207 | 29 | 60.4 | 2482 | 1 | US-08-328-254-6 | Sequence 6, Appl |
| 135 | 30 | 62.5 | 769 | 4 | US-09-949-016-10665 | Sequence 10665, A | 208 | 29 | 60.4 | 3210 | 4 | US-09-538-092-1154 | Sequence 1154, Ap |
| 136 | 30 | 62.5 | 923 | 4 | US-09-538-092-80 | Sequence 80, Appl | 209 | 29 | 60.4 | 3218 | 1 | US-08-764-100-27 | Sequence 27, Appl |
| 137 | 30 | 62.5 | 1437 | 4 | US-09-949-016-10535 | Sequence 10535, A | 210 | 29 | 60.4 | 3248 | 5 | US-08-353-700-1 | Sequence 1, Appl |
| 138 | 29 | 60.4 | 13 | 4 | US-09-082-358B-87 | Sequence 87, Appl | 211 | 29 | 60.4 | 3248 | 5 | PCT-US95-16216-1 | Sequence 2, Appl |
| 139 | 29 | 60.4 | 61 | 4 | US-09-107-532A-4643 | Sequence 4643, Ap | 212 | 28.5 | 59.4 | 180 | 4 | US-09-465-558-2 | Sequence 2, Appl |
| 140 | 29 | 60.4 | 71 | 4 | US-09-134-000C-6796 | Sequence 6796, Ap | 213 | 28.5 | 59.4 | 241 | 4 | US-09-270-767-34316 | Sequence 34316, A |
| 141 | 29 | 60.4 | 138 | 4 | US-09-252-991A-21153 | Sequence 21153, A | 214 | 28.5 | 59.4 | 241 | 4 | US-09-270-767-49533 | Sequence 49533, A |
| 142 | 29 | 60.4 | 140 | 4 | US-09-134-000C-6375 | Sequence 6375, Ap | 215 | 28.5 | 59.4 | 510 | 4 | US-09-465-558-40 | Sequence 40, Appl |
| 143 | 29 | 60.4 | 142 | 4 | US-09-902-540-12459 | Sequence 12459, A | 216 | 28 | 58.3 | 48 | 3 | US-09-346-860-10 | Sequence 10, Appl |
| 144 | 29 | 60.4 | 150 | 4 | US-09-142-108C-10 | Sequence 10, Appl | 217 | 28 | 58.3 | 48 | 3 | US-09-735-685-10 | Sequence 10, Appl |
| 145 | 29 | 60.4 | 166 | 4 | US-09-270-767-49127 | Sequence 49127, A | 218 | 28 | 58.3 | 60 | 4 | US-09-621-976-5575 | Sequence 5575, Ap |
| 146 | 29 | 60.4 | 183 | 4 | US-09-270-767-38448 | Sequence 38448, A | 219 | 28 | 58.3 | 64 | 4 | US-09-149-476-330 | Sequence 330, App |
| 147 | 29 | 60.4 | 183 | 4 | US-09-270-767-35365 | Sequence 35365, A | 220 | 28 | 58.3 | 64 | 4 | US-09-959-897-37 | Sequence 37, Appl |
| 148 | 29 | 60.4 | 186 | 4 | US-09-270-767-35570 | Sequence 35570, A | 221 | 28 | 58.3 | 72 | 4 | US-09-270-767-58180 | Sequence 58180, A |
| 149 | 29 | 60.4 | 186 | 4 | US-09-270-767-50787 | Sequence 50787, A | 222 | 28 | 58.3 | 72 | 4 | US-09-248-796A-26744 | Sequence 26744, A |
| 150 | 29 | 60.4 | 193 | 4 | US-09-543-681A-8139 | Sequence 8139, Ap | 223 | 28 | 58.3 | 76 | 4 | US-09-902-540-15288 | Sequence 15288, A |
| 151 | 29 | 60.4 | 193 | 4 | US-09-270-767-33468 | Sequence 33468, A | 224 | 28 | 58.3 | 96 | 4 | US-09-673-395A-418 | Sequence 418, App |
| 152 | 29 | 60.4 | 204 | 4 | US-09-270-767-32818 | Sequence 32818, A | 225 | 28 | 58.3 | 96 | 4 | US-09-270-767-59736 | Sequence 463, App |
| 153 | 29 | 60.4 | 204 | 4 | US-09-270-767-48035 | Sequence 48035, A | 226 | 28 | 58.3 | 107 | 4 | US-09-270-767-31878 | Sequence 31878, A |
| 154 | 29 | 60.4 | 228 | 4 | US-09-248-796A-17522 | Sequence 17522, A | 227 | 28 | 58.3 | 108 | 4 | US-09-270-767-44313 | Sequence 44313, A |
| 155 | 29 | 60.4 | 252 | 4 | US-09-489-039A-12324 | Sequence 12324, A | 228 | 28 | 58.3 | 108 | 4 | US-09-270-767-47095 | Sequence 47095, A |
| 156 | 29 | 60.4 | 254 | 4 | US-09-978-758-2 | Sequence 2, Appl | 229 | 28 | 58.3 | 108 | 4 | US-09-134-001C-4120 | Sequence 4120, Ap |
| 157 | 29 | 60.4 | 257 | 4 | US-09-540-236-2812 | Sequence 2812, Ap | 230 | 28 | 58.3 | 114 | 3 | US-08-122-546-8 | Sequence 8, Appl |
| 158 | 29 | 60.4 | 284 | 4 | US-09-489-039A-9889 | Sequence 9889, Ap | 231 | 28 | 58.3 | 116 | 1 | US-08-764-938-8 | Sequence 8, Appl |
| 159 | 29 | 60.4 | 296 | 4 | US-09-540-236-2650 | Sequence 2650, Ap | 232 | 28 | 58.3 | 116 | 3 | US-09-131-052-8 | Sequence 8, Appl |
| 160 | 29 | 60.4 | 311 | 4 | US-09-270-767-33374 | Sequence 33374, A | 233 | 28 | 58.3 | 116 | 3 | US-09-489-039A-11787 | Sequence 8, Appl |
| 161 | 29 | 60.4 | 311 | 4 | US-09-270-767-48591 | Sequence 48591, A | 234 | 28 | 58.3 | 123 | 4 | US-09-252-991A-22501 | Sequence 9, Appl |
| 162 | 29 | 60.4 | 313 | 4 | US-09-248-796A-17621 | Sequence 17621, A | 235 | 28 | 58.3 | 137 | 4 | US-09-270-767-32176 | Sequence 32176, A |
| 163 | 29 | 60.4 | 318 | 4 | US-09-107-532A-5738 | Sequence 5738, Ap | 236 | 28 | 58.3 | 150 | 4 | US-09-318-947A-9 | Sequence 9, Appl |
| 164 | 29 | 60.4 | 318 | 4 | US-09-540-236-3585 | Sequence 3585, Ap | 237 | 28 | 58.3 | 150 | 4 | US-08-795-303-9 | Sequence 4039A, A |
| 165 | 29 | 60.4 | 329 | 4 | US-08-981-527A-8 | Sequence 8, Appl | 238 | 28 | 58.3 | 151 | 1 | US-09-270-767-55610 | Sequence 55610, A |
| 166 | 29 | 60.4 | 329 | 4 | US-10-147-936B-8 | Sequence 5, Appl | 239 | 28 | 58.3 | 151 | 2 | US-09-270-767-14827 | Sequence 14827, A |
| 167 | 29 | 60.4 | 346 | 3 | US-09-393-554-5 | Sequence 25822, A | 240 | 28 | 58.3 | 155 | 4 | US-09-902-540-12974 | Sequence 12974, A |
| 168 | 29 | 60.4 | 346 | 4 | US-09-248-796A-25822 | Sequence 17746, A | 241 | 28 | 58.3 | 155 | 4 | US-09-583-110-4824 | Sequence 4824, Ap |
| 169 | 29 | 60.4 | 350 | 4 | US-09-248-796A-17746 | Sequence 17746, A | 242 | 28 | 58.3 | 155 | 4 | | |
| 170 | 29 | 60.4 | 377 | 1 | US-08-153-848-42 | Sequence 42, Appl | 243 | 28 | 58.3 | 156 | 4 | | |
| 171 | 29 | 60.4 | 377 | 3 | US-09-299-843A-42 | Sequence 42, Appl | 244 | 28 | 58.3 | 201 | 4 | | |
| 172 | 29 | 60.4 | 377 | 3 | US-09-088-337B-42 | Sequence 42, Appl | 245 | 28 | 58.3 | 201 | 4 | | |
| 173 | 29 | 60.4 | 377 | 5 | PCT-US93-11153-42 | Sequence 42, Appl | 246 | 28 | 58.3 | 204 | 4 | | |

| | | | | | | | | | | | | | |
|-----|-----|------|-----|---|----------------------|--------------------|-----|------|------|------|---|----------------------|--------------------|
| 247 | 208 | 58.3 | 208 | 4 | US-09-673-395A-516 | Sequence 516, App | 320 | 28 | 58.3 | 855 | 4 | US-09-107-532A-5646 | Sequence 5646, Ap |
| 248 | 220 | 58.3 | 220 | 4 | US-09-252-991A-21239 | Sequence 21239, A | 321 | 28 | 58.3 | 858 | 4 | US-09-252-991A-23178 | Sequence 23178, A |
| 249 | 226 | 58.3 | 226 | 4 | US-09-328-352-598A | Sequence 598A, Ap | 322 | 28 | 58.3 | 890 | 1 | US-08-472-934-8 | Sequence 8, Appli |
| 250 | 237 | 58.3 | 237 | 4 | US-09-583-110-5199 | Sequence 5199, Ap | 323 | 28 | 58.3 | 890 | 2 | US-08-323-460A-8 | Sequence 8, Appli |
| 251 | 241 | 58.3 | 241 | 4 | US-09-107-433-3412 | Sequence 3412, Ap | 324 | 28 | 58.3 | 890 | 2 | US-08-461-146C-8 | Sequence 8, Appli |
| 252 | 244 | 58.3 | 244 | 4 | US-09-902-540-16220 | Sequence 16220, A | 325 | 28 | 58.3 | 890 | 3 | US-08-461-145C-8 | Sequence 12, Appli |
| 253 | 254 | 58.3 | 254 | 4 | US-09-252-991A-25576 | Sequence 25576, A | 326 | 28 | 58.3 | 890 | 3 | US-08-628-829-12 | Sequence 12, Appli |
| 254 | 264 | 58.3 | 264 | 4 | US-09-270-767-33544 | Sequence 33544, A | 327 | 28 | 58.3 | 910 | 4 | US-09-949-016-7055 | Sequence 7055, Ap |
| 255 | 265 | 58.3 | 265 | 3 | US-09-154-083-8 | Sequence 8, Appli | 328 | 28 | 58.3 | 977 | 4 | US-09-580-656-1 | Sequence 1, Appli |
| 256 | 268 | 58.3 | 268 | 4 | US-09-252-991A-21630 | Sequence 21630, A | 329 | 28 | 58.3 | 977 | 4 | US-09-733-764-1 | Sequence 1, Appli |
| 257 | 272 | 58.3 | 272 | 4 | US-09-949-016-6331 | Sequence 6331, Ap | 330 | 28 | 58.3 | 985 | 2 | US-08-867-941-13 | Sequence 13, Appli |
| 258 | 276 | 58.3 | 276 | 4 | US-09-949-016-6331 | Sequence 6331, Ap | 331 | 28 | 58.3 | 985 | 2 | US-08-867-941-17 | Sequence 17, Appli |
| 259 | 296 | 58.3 | 296 | 4 | US-09-270-767-42861 | Sequence 42861, A | 332 | 28 | 58.3 | 985 | 3 | US-09-074-658-13 | Sequence 13, Appli |
| 260 | 300 | 58.3 | 300 | 4 | US-09-252-991A-23342 | Sequence 23342, A | 333 | 28 | 58.3 | 985 | 3 | US-09-074-658-17 | Sequence 17, Appli |
| 261 | 331 | 58.3 | 331 | 4 | US-09-546-986A-4 | Sequence 4, Appli | 334 | 28 | 58.3 | 1000 | 2 | US-08-867-941-12 | Sequence 12, Appli |
| 262 | 331 | 58.3 | 331 | 4 | US-09-524-730-4 | Sequence 730, A | 335 | 28 | 58.3 | 1000 | 2 | US-08-867-941-16 | Sequence 16, Appli |
| 263 | 332 | 58.3 | 332 | 4 | US-09-949-016-10159 | Sequence 10159, A | 336 | 28 | 58.3 | 1000 | 3 | US-09-074-658-12 | Sequence 12, Appli |
| 264 | 341 | 58.3 | 341 | 4 | US-09-252-991A-22453 | Sequence 22453, A | 337 | 28 | 58.3 | 1003 | 4 | US-09-074-658-16 | Sequence 16, Appli |
| 265 | 342 | 58.3 | 342 | 4 | US-09-248-796A-19527 | Sequence 19527, A | 338 | 28 | 58.3 | 1003 | 4 | US-09-540-236-2757 | Sequence 2757, Ap |
| 266 | 344 | 58.3 | 344 | 4 | US-09-248-796A-19527 | Sequence 19527, A | 339 | 28 | 58.3 | 1101 | 2 | US-08-469-537A-96 | Sequence 96, Appli |
| 267 | 375 | 58.3 | 375 | 4 | US-09-902-540-12456 | Sequence 12456, A | 340 | 28 | 58.3 | 1118 | 1 | US-07-934-333B-2 | Sequence 2, Appli |
| 268 | 392 | 58.3 | 392 | 4 | US-09-071-035-260 | Sequence 260, App | 341 | 28 | 58.3 | 1118 | 1 | US-08-278-089A-2 | Sequence 2, Appli |
| 269 | 394 | 58.3 | 394 | 4 | US-09-949-016-6716 | Sequence 6716, Ap | 342 | 28 | 58.3 | 1118 | 2 | US-08-838-957A-2 | Sequence 6, Appli |
| 270 | 404 | 58.3 | 404 | 1 | US-08-696-770-2 | Sequence 2, Appli | 343 | 28 | 58.3 | 1122 | 2 | US-08-838-957A-6 | Sequence 6, Appli |
| 271 | 404 | 58.3 | 404 | 2 | US-09-015-557-2 | Sequence 2, Appli | 344 | 28 | 58.3 | 1122 | 2 | US-08-323-474-2 | Sequence 2, Appli |
| 272 | 408 | 58.3 | 408 | 4 | US-09-583-110-5062 | Sequence 5062, Ap | 345 | 28 | 58.3 | 1124 | 1 | US-09-949-016-5946 | Sequence 5946, Ap |
| 273 | 410 | 58.3 | 410 | 4 | US-09-489-039A-7598 | Sequence 7598, Ap | 346 | 28 | 58.3 | 1124 | 5 | PCT-US93-06093-2 | Sequence 2, Appli |
| 274 | 416 | 58.3 | 416 | 3 | US-08-978-289-12 | Sequence 12, Appli | 347 | 28 | 58.3 | 1124 | 5 | PCT-US93-06093-2 | Sequence 2, Appli |
| 275 | 416 | 58.3 | 416 | 4 | US-09-601-478-1 | Sequence 1, Appli | 348 | 28 | 58.3 | 1157 | 4 | US-09-949-016-9568 | Sequence 9568, Ap |
| 276 | 416 | 58.3 | 416 | 4 | US-09-601-478-4 | Sequence 4, Appli | 349 | 28 | 58.3 | 1157 | 4 | US-09-583-110-3634 | Sequence 3634, Ap |
| 277 | 417 | 58.3 | 417 | 4 | US-09-252-991A-20165 | Sequence 20165, A | 350 | 28 | 58.3 | 1203 | 4 | US-09-107-433-4255 | Sequence 4255, Ap |
| 278 | 418 | 58.3 | 418 | 4 | US-09-489-039A-11946 | Sequence 11946, A | 351 | 28 | 58.3 | 1203 | 4 | US-09-107-433-4255 | Sequence 10, Appli |
| 279 | 423 | 58.3 | 423 | 4 | US-09-107-433-2664 | Sequence 2664, Ap | 352 | 28 | 58.3 | 1247 | 2 | US-08-323-460A-10 | Sequence 10, Appli |
| 280 | 424 | 58.3 | 424 | 4 | US-09-796-487-8 | Sequence 8, Appli | 353 | 28 | 58.3 | 1247 | 2 | US-08-461-146C-10 | Sequence 10, Appli |
| 281 | 427 | 58.3 | 427 | 4 | US-09-949-016-9842 | Sequence 9842, Ap | 354 | 28 | 58.3 | 1247 | 3 | US-08-461-145C-10 | Sequence 10, Appli |
| 282 | 431 | 58.3 | 431 | 4 | US-09-543-681A-6326 | Sequence 6326, Ap | 355 | 28 | 58.3 | 1275 | 4 | US-09-902-540-10769 | Sequence 10769, A |
| 283 | 437 | 58.3 | 437 | 4 | US-09-252-991A-18636 | Sequence 18636, Ap | 356 | 28 | 58.3 | 1279 | 4 | US-09-170-496D-293 | Sequence 293, App |
| 284 | 440 | 58.3 | 440 | 4 | US-09-252-991A-26855 | Sequence 26855, A | 357 | 28 | 58.3 | 1279 | 4 | US-09-364-425B-58 | Sequence 58, Appli |
| 285 | 440 | 58.3 | 440 | 4 | US-09-489-039A-12067 | Sequence 12067, A | 358 | 28 | 58.3 | 1326 | 4 | US-09-489-039A-7584 | Sequence 7584, Ap |
| 286 | 443 | 58.3 | 443 | 4 | US-09-107-532A-6063 | Sequence 6063, Ap | 359 | 28 | 58.3 | 1330 | 4 | US-09-543-681A-8057 | Sequence 8057, Ap |
| 287 | 448 | 58.3 | 448 | 4 | US-09-361-443-4 | Sequence 4, Appli | 360 | 28 | 58.3 | 1339 | 3 | US-08-462-467B-14 | Sequence 14, Appli |
| 288 | 461 | 58.3 | 461 | 4 | US-09-252-991A-26351 | Sequence 26351, A | 361 | 28 | 58.3 | 1431 | 4 | US-09-902-540-10614 | Sequence 10614, A |
| 289 | 467 | 58.3 | 467 | 4 | US-09-361-443-2 | Sequence 2, Appli | 362 | 28 | 58.3 | 1462 | 4 | US-09-538-092-1043 | Sequence 1043, Ap |
| 290 | 469 | 58.3 | 469 | 4 | US-09-198-452A-793 | Sequence 793, App | 363 | 28 | 58.3 | 1495 | 3 | US-08-462-467B-12 | Sequence 12, Appli |
| 291 | 470 | 58.3 | 470 | 4 | US-09-438-185A-745 | Sequence 745, App | 364 | 28 | 58.3 | 1514 | 2 | US-08-853-310-4 | Sequence 4, Appli |
| 292 | 470 | 58.3 | 470 | 4 | US-09-543-681A-5952 | Sequence 5952, Ap | 365 | 28 | 58.3 | 1597 | 3 | US-09-423-890-13 | Sequence 13, Appli |
| 293 | 473 | 58.3 | 473 | 4 | US-09-949-016-9481 | Sequence 9481, Ap | 366 | 28 | 58.3 | 1597 | 3 | US-08-628-829-14 | Sequence 14, Appli |
| 294 | 517 | 58.3 | 517 | 4 | US-09-142-108C-21 | Sequence 21, Appli | 367 | 28 | 58.3 | 1638 | 4 | US-09-071-035-258 | Sequence 258, App |
| 295 | 543 | 58.3 | 543 | 4 | US-09-248-796A-14702 | Sequence 14702, A | 368 | 28 | 58.3 | 1638 | 4 | US-09-071-035-282 | Sequence 282, App |
| 296 | 553 | 58.3 | 553 | 1 | US-08-565-386-12 | Sequence 12, Appli | 369 | 28 | 58.3 | 1638 | 4 | US-09-071-035-282 | Sequence 282, App |
| 297 | 574 | 58.3 | 574 | 4 | US-09-252-991A-30868 | Sequence 30868, A | 370 | 28 | 58.3 | 1747 | 4 | US-09-134-000C-5999 | Sequence 5999, Ap |
| 298 | 579 | 58.3 | 579 | 4 | US-09-543-681A-5050 | Sequence 5050, Ap | 371 | 28 | 58.3 | 1996 | 2 | US-08-804-198-3 | Sequence 3, Appli |
| 299 | 585 | 58.3 | 585 | 2 | US-08-867-941-21 | Sequence 21, Appli | 372 | 28 | 58.3 | 1996 | 2 | US-08-804-198-3 | Sequence 3, Appli |
| 300 | 585 | 58.3 | 585 | 3 | US-09-074-658-21 | Sequence 21, Appli | 373 | 28 | 58.3 | 2432 | 3 | US-09-074-658-15 | Sequence 15, Appli |
| 301 | 596 | 58.3 | 596 | 3 | US-09-171-337A-6 | Sequence 6, Appli | 374 | 28 | 58.3 | 2432 | 3 | US-09-074-658-11 | Sequence 11, Appli |
| 302 | 596 | 58.3 | 596 | 4 | US-09-631-022-6 | Sequence 6, Appli | 375 | 28 | 58.3 | 2451 | 4 | US-09-949-016-9675 | Sequence 9675, Ap |
| 303 | 651 | 58.3 | 651 | 4 | US-09-134-000C-4516 | Sequence 4516, Ap | 376 | 28 | 58.3 | 2451 | 4 | US-09-949-016-9675 | Sequence 15, Appli |
| 304 | 667 | 58.3 | 667 | 4 | US-09-902-540-11066 | Sequence 11066, A | 377 | 28 | 58.3 | 2787 | 3 | US-09-245-041-15 | Sequence 15, Appli |
| 305 | 669 | 58.3 | 669 | 4 | US-09-710-279-198 | Sequence 198, App | 378 | 28 | 58.3 | 2787 | 4 | US-09-358-055B-15 | Sequence 15, Appli |
| 306 | 681 | 58.3 | 681 | 3 | US-09-071-035-264 | Sequence 264, App | 379 | 28 | 58.3 | 3562 | 4 | US-09-893-238-15 | Sequence 15, Appli |
| 307 | 681 | 58.3 | 681 | 3 | US-08-760-615-6 | Sequence 6, Appli | 380 | 28 | 58.3 | 3562 | 4 | US-09-679-279-14 | Sequence 14, Appli |
| 308 | 684 | 58.3 | 684 | 4 | US-09-252-991A-24802 | Sequence 24802, A | 381 | 28 | 58.3 | 3567 | 2 | US-07-642-734C-4 | Sequence 4, Appli |
| 309 | 704 | 58.3 | 704 | 4 | US-09-590-656-2 | Sequence 2, Appli | 382 | 28 | 58.3 | 3567 | 3 | US-08-439-009A-4 | Sequence 4, Appli |
| 310 | 711 | 58.3 | 711 | 3 | US-08-949-588-2 | Sequence 2, Appli | 383 | 28 | 58.3 | 3567 | 3 | US-08-439-009A-4 | Sequence 4, Appli |
| 311 | 723 | 58.3 | 723 | 3 | US-09-134-001C-5060 | Sequence 5060, Ap | 384 | 28 | 58.3 | 3567 | 3 | US-08-804-227C-8 | Sequence 8, Appli |
| 312 | 749 | 58.3 | 749 | 4 | US-09-562-737-97 | Sequence 97, Appli | 385 | 28 | 58.3 | 3567 | 3 | US-08-804-227C-14 | Sequence 14, Appli |
| 313 | 753 | 58.3 | 753 | 2 | US-08-867-941-20 | Sequence 20, Appli | 386 | 27.5 | 57.3 | 239 | 4 | US-09-902-540-16789 | Sequence 16789, A |
| 314 | 753 | 58.3 | 753 | 3 | US-09-074-658-20 | Sequence 20, Appli | 387 | 27.5 | 57.3 | 293 | 4 | US-09-902-540-14362 | Sequence 14362, A |
| 315 | 792 | 58.3 | 792 | 3 | US-09-543-681A-6617 | Sequence 6617, Ap | 388 | 27.5 | 57.3 | 402 | 3 | US-09-292-097-16 | Sequence 16, Appli |
| 316 | 796 | 58.3 | 796 | 3 | US-09-005-180A-1 | Sequence 1, Appli | 389 | 27.5 | 57.3 | 402 | 3 | US-09-933-561-16 | Sequence 16, Appli |
| 317 | 820 | 58.3 | 820 | 4 | US-09-902-540-16384 | Sequence 16384, A | 390 | 27.5 | 57.3 | 476 | 4 | US-09-248-796A-17464 | Sequence 17464, A |
| 318 | 832 | 58.3 | 832 | 4 | US-09-252-991A-24866 | Sequence 24866, A | 391 | 27.5 | 57.3 | 1558 | 4 | US-09-949-016-6803 | Sequence 6803, Ap |
| 319 | | 58.3 | | | | | 392 | 27.5 | 57.3 | 1606 | 4 | US-09-949-016-7371 | Sequence 7371, Ap |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|----------------------|-------------------|-----|----|------|-----|---|----------------------|--------------------|
| 393 | 27 | 56.2 | 14 | 3 | US-09-306-756-2 | Sequence 2, Appli | 466 | 27 | 56.2 | 300 | 2 | US-08-794-796-2 | Sequence 2, Appli |
| 394 | 27 | 56.2 | 14 | 4 | US-09-674-307-2 | Sequence 2, Appli | 467 | 27 | 56.2 | 300 | 4 | US-09-585-858-45 | Sequence 45, Appli |
| 395 | 27 | 56.2 | 62 | 3 | US-08-936-165A-364 | Sequence 364, App | 468 | 27 | 56.2 | 300 | 4 | US-09-632-277A-2 | Sequence 2, Appli |
| 396 | 27 | 56.2 | 64 | 4 | US-09-248-796A-27846 | Sequence 27846, A | 469 | 27 | 56.2 | 300 | 4 | US-09-523-323-52 | Sequence 52, Appli |
| 397 | 27 | 56.2 | 75 | 4 | US-09-270-767-58435 | Sequence 58435, A | 470 | 27 | 56.2 | 300 | 4 | US-09-896-096A-1 | Sequence 1, Appli |
| 398 | 27 | 56.2 | 79 | 3 | US-09-100-802-4 | Sequence 4, Appli | 471 | 27 | 56.2 | 300 | 4 | US-10-270-878-45 | Sequence 45, Appli |
| 399 | 27 | 56.2 | 83 | 4 | US-09-248-796A-26718 | Sequence 26718, A | 472 | 27 | 56.2 | 300 | 4 | US-09-936-019-3 | Sequence 3, Appli |
| 400 | 27 | 56.2 | 85 | 4 | US-09-270-767-61052 | Sequence 61052, A | 473 | 27 | 56.2 | 300 | 3 | US-09-002-298-3 | Sequence 3, Appli |
| 401 | 27 | 56.2 | 88 | 2 | US-08-465-380-43 | Sequence 43, Appl | 474 | 27 | 56.2 | 301 | 4 | US-09-481-277-3 | Sequence 3, Appli |
| 402 | 27 | 56.2 | 88 | 2 | US-08-486-397-43 | Sequence 43, Appl | 475 | 27 | 56.2 | 301 | 4 | US-09-252-991A-27392 | Sequence 27392, A |
| 403 | 27 | 56.2 | 88 | 2 | US-08-486-399-43 | Sequence 43, Appl | 476 | 27 | 56.2 | 301 | 4 | US-08-311-731A-308 | Sequence 308, App |
| 404 | 27 | 56.2 | 88 | 2 | US-08-461-965-43 | Sequence 43, Appl | 477 | 27 | 56.2 | 301 | 4 | US-09-270-767-35774 | Sequence 35774, A |
| 405 | 27 | 56.2 | 88 | 2 | US-08-634-641-43 | Sequence 43, Appl | 478 | 27 | 56.2 | 301 | 4 | US-09-270-767-75091 | Sequence 75091, A |
| 406 | 27 | 56.2 | 88 | 3 | US-09-249-471-43 | Sequence 43, Appl | 479 | 27 | 56.2 | 309 | 4 | US-09-415-260A-1 | Sequence 1, Appli |
| 407 | 27 | 56.2 | 88 | 3 | US-09-249-472-43 | Sequence 43, Appl | 480 | 27 | 56.2 | 309 | 4 | US-09-415-260A-2 | Sequence 2, Appli |
| 408 | 27 | 56.2 | 88 | 3 | US-09-249-451-43 | Sequence 43, Appl | 481 | 27 | 56.2 | 309 | 4 | US-09-415-260A-3 | Sequence 3, Appli |
| 409 | 27 | 56.2 | 88 | 3 | US-08-809-455-43 | Sequence 43, Appl | 482 | 27 | 56.2 | 309 | 4 | US-09-415-260A-4 | Sequence 4, Appli |
| 410 | 27 | 56.2 | 88 | 3 | US-09-249-461-43 | Sequence 43, Appl | 483 | 27 | 56.2 | 309 | 4 | US-09-415-260A-5 | Sequence 5, Appli |
| 411 | 27 | 56.2 | 88 | 3 | US-09-249-448-43 | Sequence 43, Appl | 484 | 27 | 56.2 | 309 | 4 | US-09-415-260A-6 | Sequence 6, Appli |
| 412 | 27 | 56.2 | 88 | 4 | US-09-249-473-43 | Sequence 43, Appl | 485 | 27 | 56.2 | 309 | 4 | US-09-415-260A-7 | Sequence 7, Appli |
| 413 | 27 | 56.2 | 97 | 4 | US-09-270-767-46651 | Sequence 46651, A | 486 | 27 | 56.2 | 309 | 4 | US-09-415-260A-8 | Sequence 8, Appli |
| 414 | 27 | 56.2 | 102 | 4 | US-09-902-540-14150 | Sequence 14150, A | 487 | 27 | 56.2 | 313 | 4 | US-09-602-777A-190 | Sequence 190, App |
| 415 | 27 | 56.2 | 105 | 4 | US-09-540-236-2606 | Sequence 2606, Ap | 488 | 27 | 56.2 | 313 | 4 | US-09-602-777A-440 | Sequence 440, App |
| 416 | 27 | 56.2 | 111 | 4 | US-09-270-767-33866 | Sequence 33866, A | 489 | 27 | 56.2 | 315 | 4 | US-09-543-681A-7121 | Sequence 7121, Ap |
| 417 | 27 | 56.2 | 111 | 4 | US-09-270-767-49083 | Sequence 49083, A | 490 | 27 | 56.2 | 315 | 4 | US-09-270-767-33342 | Sequence 33342, A |
| 418 | 27 | 56.2 | 118 | 3 | US-08-301-162-10 | Sequence 10, Appl | 491 | 27 | 56.2 | 315 | 4 | US-09-270-767-48559 | Sequence 48559, A |
| 419 | 27 | 56.2 | 118 | 3 | US-08-461-240-10 | Sequence 10, Appl | 492 | 27 | 56.2 | 325 | 1 | US-07-626-589-2 | Sequence 2, Appli |
| 420 | 27 | 56.2 | 118 | 4 | US-09-968-927-10 | Sequence 10, Appl | 493 | 27 | 56.2 | 325 | 1 | US-08-190-082A-57 | Sequence 57, Appl |
| 421 | 27 | 56.2 | 126 | 1 | US-08-044-547-3 | Sequence 3, Appli | 494 | 27 | 56.2 | 325 | 1 | US-08-323-444A-1 | Sequence 1, Appli |
| 422 | 27 | 56.2 | 129 | 4 | US-09-107-532A-6426 | Sequence 6426, Ap | 495 | 27 | 56.2 | 325 | 1 | US-08-236-410-2 | Sequence 2, Appli |
| 423 | 27 | 56.2 | 130 | 4 | US-09-902-540-11863 | Sequence 11863, A | 496 | 27 | 56.2 | 325 | 1 | US-08-465-421-2 | Sequence 2, Appli |
| 424 | 27 | 56.2 | 139 | 4 | US-09-270-767-38418 | Sequence 38418, A | 497 | 27 | 56.2 | 325 | 3 | US-08-477-346-57 | Sequence 57, Appl |
| 425 | 27 | 56.2 | 139 | 4 | US-09-270-767-53635 | Sequence 53635, A | 498 | 27 | 56.2 | 325 | 3 | US-08-473-089-57 | Sequence 57, Appl |
| 426 | 27 | 56.2 | 141 | 4 | US-09-489-039A-9720 | Sequence 9720, Ap | 499 | 27 | 56.2 | 325 | 4 | US-08-487-072A-57 | Sequence 57, Appl |
| 427 | 27 | 56.2 | 145 | 4 | US-09-732-210-1321 | Sequence 1321, Ap | 500 | 27 | 56.2 | 326 | 4 | US-09-198-452A-150 | Sequence 150, App |
| 428 | 27 | 56.2 | 146 | 4 | US-09-893-737-88 | Sequence 88, Appl | 501 | 27 | 56.2 | 326 | 4 | US-09-438-185A-134 | Sequence 134, App |
| 429 | 27 | 56.2 | 146 | 4 | US-09-523-323-59 | Sequence 59, Appl | 502 | 27 | 56.2 | 326 | 4 | US-09-902-540-11608 | Sequence 11608, A |
| 430 | 27 | 56.2 | 147 | 1 | US-08-044-547-1 | Sequence 1, Appli | 503 | 27 | 56.2 | 330 | 4 | US-09-107-532A-7050 | Sequence 7050, Ap |
| 431 | 27 | 56.2 | 149 | 4 | US-09-270-767-47885 | Sequence 47885, A | 504 | 27 | 56.2 | 333 | 4 | US-09-949-016-7678 | Sequence 7678, Ap |
| 432 | 27 | 56.2 | 153 | 3 | US-09-286-529-2 | Sequence 2, Appli | 505 | 27 | 56.2 | 338 | 4 | US-09-252-991A-26745 | Sequence 26745, A |
| 433 | 27 | 56.2 | 153 | 4 | US-09-270-767-3444 | Sequence 3444, A | 506 | 27 | 56.2 | 338 | 4 | US-09-949-016-7050 | Sequence 7050, Ap |
| 434 | 27 | 56.2 | 153 | 4 | US-09-270-767-49661 | Sequence 49661, A | 507 | 27 | 56.2 | 338 | 4 | US-09-902-540-13885 | Sequence 13885, A |
| 435 | 27 | 56.2 | 156 | 4 | US-09-270-767-32472 | Sequence 32472, A | 508 | 27 | 56.2 | 346 | 4 | US-09-252-991A-31465 | Sequence 31465, A |
| 436 | 27 | 56.2 | 156 | 4 | US-09-270-767-47689 | Sequence 47689, A | 509 | 27 | 56.2 | 348 | 4 | US-09-489-039A-8827 | Sequence 8827, Ap |
| 437 | 27 | 56.2 | 162 | 4 | US-09-328-352-5894 | Sequence 5894, Ap | 510 | 27 | 56.2 | 351 | 4 | US-09-902-540-12944 | Sequence 12944, A |
| 438 | 27 | 56.2 | 163 | 4 | US-09-465-558-8 | Sequence 8, Appli | 511 | 27 | 56.2 | 352 | 4 | US-09-252-991A-19989 | Sequence 19989, A |
| 439 | 27 | 56.2 | 170 | 3 | US-09-189-035-2 | Sequence 2, Appli | 512 | 27 | 56.2 | 352 | 4 | US-09-711-164-448 | Sequence 448, App |
| 440 | 27 | 56.2 | 171 | 4 | US-09-382-086-2 | Sequence 2, Appli | 513 | 27 | 56.2 | 353 | 4 | US-09-902-540-14186 | Sequence 14186, A |
| 441 | 27 | 56.2 | 171 | 4 | US-09-489-039A-8636 | Sequence 8636, Ap | 514 | 27 | 56.2 | 356 | 3 | US-09-235-103-4 | Sequence 4, Appli |
| 442 | 27 | 56.2 | 173 | 4 | US-09-252-991A-25090 | Sequence 25090, A | 515 | 27 | 56.2 | 356 | 3 | US-09-235-103-13 | Sequence 13, Appli |
| 443 | 27 | 56.2 | 182 | 4 | US-10-085-572-8 | Sequence 8, Appli | 516 | 27 | 56.2 | 363 | 4 | US-09-270-767-45543 | Sequence 45543, A |
| 444 | 27 | 56.2 | 182 | 4 | US-10-087-195-8 | Sequence 8, Appli | 517 | 27 | 56.2 | 363 | 4 | US-09-949-016-9869 | Sequence 9869, Ap |
| 445 | 27 | 56.2 | 184 | 4 | US-09-270-767-43100 | Sequence 43100, A | 518 | 27 | 56.2 | 364 | 4 | US-09-270-767-42122 | Sequence 42122, A |
| 446 | 27 | 56.2 | 191 | 4 | US-09-538-092-140 | Sequence 140, App | 519 | 27 | 56.2 | 368 | 4 | US-09-614-912-38 | Sequence 38, Appl |
| 447 | 27 | 56.2 | 193 | 4 | US-09-902-540-11304 | Sequence 11304, A | 520 | 27 | 56.2 | 368 | 4 | US-09-248-796A-20840 | Sequence 20840, A |
| 448 | 27 | 56.2 | 200 | 4 | US-09-618-919A-20 | Sequence 20, Appl | 521 | 27 | 56.2 | 370 | 3 | US-09-134-001C-3769 | Sequence 3769, Ap |
| 449 | 27 | 56.2 | 206 | 4 | US-09-252-991A-17940 | Sequence 17940, A | 522 | 27 | 56.2 | 372 | 4 | US-09-328-352-6955 | Sequence 6955, Ap |
| 450 | 27 | 56.2 | 209 | 4 | US-09-489-039A-13956 | Sequence 13956, A | 523 | 27 | 56.2 | 376 | 3 | US-09-056-556-202 | Sequence 202, App |
| 451 | 27 | 56.2 | 211 | 3 | US-09-286-529-20 | Sequence 20, Appl | 524 | 27 | 56.2 | 376 | 4 | US-09-072-596-197 | Sequence 197, App |
| 452 | 27 | 56.2 | 218 | 4 | US-09-248-796A-15868 | Sequence 15868, A | 525 | 27 | 56.2 | 376 | 4 | US-09-072-967-202 | Sequence 202, App |
| 453 | 27 | 56.2 | 233 | 2 | US-09-151-611-1 | Sequence 1, Appli | 526 | 27 | 56.2 | 379 | 4 | US-09-491-577-14 | Sequence 14, Appl |
| 454 | 27 | 56.2 | 233 | 3 | US-09-370-102-1 | Sequence 1, Appli | 527 | 27 | 56.2 | 379 | 4 | US-09-602-777A-112 | Sequence 112, App |
| 455 | 27 | 56.2 | 245 | 4 | US-08-311-731A-119 | Sequence 119, App | 528 | 27 | 56.2 | 389 | 4 | US-09-710-279-618 | Sequence 618, App |
| 456 | 27 | 56.2 | 249 | 4 | US-09-543-681A-6859 | Sequence 6859, Ap | 529 | 27 | 56.2 | 391 | 4 | US-09-252-991A-17690 | Sequence 17690, A |
| 457 | 27 | 56.2 | 264 | 2 | US-07-857-224B-67 | Sequence 67, Appl | 530 | 27 | 56.2 | 409 | 4 | US-09-538-092-1214 | Sequence 1214, Ap |
| 458 | 27 | 56.2 | 267 | 4 | US-09-248-796A-16355 | Sequence 16355, A | 531 | 27 | 56.2 | 409 | 4 | US-09-949-016-6281 | Sequence 6281, Ap |
| 459 | 27 | 56.2 | 268 | 2 | US-07-857-224B-33 | Sequence 33, Appl | 532 | 27 | 56.2 | 419 | 3 | US-08-974-691-3 | Sequence 3, Appli |
| 460 | 27 | 56.2 | 269 | 4 | US-09-252-991A-29917 | Sequence 29917, A | 533 | 27 | 56.2 | 419 | 4 | US-09-705-448-10 | Sequence 10, Appl |
| 461 | 27 | 56.2 | 270 | 3 | US-09-134-001C-4376 | Sequence 4376, Ap | 534 | 27 | 56.2 | 427 | 4 | US-09-134-000C-4847 | Sequence 4847, Ap |
| 462 | 27 | 56.2 | 271 | 4 | US-09-936-019-1 | Sequence 1, Appli | 535 | 27 | 56.2 | 430 | 1 | US-08-785-076-3 | Sequence 3, Appli |
| 463 | 27 | 56.2 | 272 | 4 | US-09-328-352-7112 | Sequence 7112, Ap | 536 | 27 | 56.2 | 430 | 1 | US-09-018-824-3 | Sequence 3, Appli |
| 464 | 27 | 56.2 | 291 | 4 | US-09-902-540-15646 | Sequence 15646, A | 537 | 27 | 56.2 | 430 | 4 | US-09-489-039A-10370 | Sequence 10370, A |
| 465 | 27 | 56.2 | 299 | 3 | US-09-286-529-17 | Sequence 17, Appl | 538 | 27 | 56.2 | 432 | 1 | US-08-785-076-2 | Sequence 2, Appli |

| | | | | | | | | | | | | |
|-----|----|------|------|---|----------------------|--------------------|-----|------|------|-----|----------------------|--------------------|
| 539 | 27 | 56.2 | 432 | 4 | US-09-018-824-2 | Sequence 2, Appli | 612 | 27 | 56.2 | 3 | US-08-695-651-6 | Sequence 6, Appli |
| 540 | 27 | 56.2 | 434 | 4 | US-09-198-452A-118 | Sequence 118, App | 613 | 27 | 56.2 | 3 | US-08-930-285-6 | Sequence 6, Appli |
| 541 | 27 | 56.2 | 434 | 4 | US-09-438-185A-102 | Sequence 102, App | 614 | 27 | 56.2 | 3 | US-08-695-421-6 | Sequence 10, Appli |
| 542 | 27 | 56.2 | 438 | 3 | US-09-134-001C-3139 | Sequence 3139, Ap | 615 | 27 | 56.2 | 3 | US-08-697-826A-10 | Sequence 2, Appli |
| 543 | 27 | 56.2 | 442 | 4 | US-09-489-039A-12384 | Sequence 12384, Ap | 616 | 27 | 56.2 | 3 | US-08-462-467B-2 | Sequence 8, Appli |
| 544 | 27 | 56.2 | 446 | 3 | US-09-761-716-2 | Sequence 2, Appli | 617 | 27 | 56.2 | 3 | US-08-462-467B-8 | Sequence 10, Appli |
| 545 | 27 | 56.2 | 449 | 4 | US-09-134-000C-4588 | Sequence 4588, Ap | 618 | 27 | 56.2 | 3 | US-09-081-501B-10 | Sequence 1136, Ap |
| 546 | 27 | 56.2 | 454 | 4 | US-09-949-016-11120 | Sequence 11120, A | 619 | 27 | 56.2 | 3 | US-09-538-092-1136 | Sequence 420, App |
| 547 | 27 | 56.2 | 460 | 4 | US-09-902-540-13166 | Sequence 32040, A | 620 | 27 | 56.2 | 4 | US-09-854-133-425 | Sequence 70, Appli |
| 548 | 27 | 56.2 | 465 | 4 | US-09-902-540-14925 | Sequence 14925, A | 621 | 27 | 56.2 | 4 | US-09-919-497-70 | Sequence 2, Appli |
| 549 | 27 | 56.2 | 472 | 4 | US-09-902-540-14925 | Sequence 14925, A | 622 | 27 | 56.2 | 4 | US-09-424-783-3 | Sequence 3, Appli |
| 550 | 27 | 56.2 | 475 | 4 | US-09-107-532A-3866 | Sequence 3866, Ap | 623 | 27 | 56.2 | 4 | US-09-424-783-5 | Sequence 5, Appli |
| 551 | 27 | 56.2 | 478 | 4 | US-09-252-991A-32557 | Sequence 32557, A | 624 | 27 | 56.2 | 4 | US-09-538-092-979 | Sequence 79, App |
| 552 | 27 | 56.2 | 489 | 3 | US-09-134-001C-4902 | Sequence 4902, Ap | 625 | 27 | 56.2 | 4 | US-09-424-783-4 | Sequence 4, Appli |
| 553 | 27 | 56.2 | 512 | 4 | US-09-142-108C-6 | Sequence 6, Appli | 626 | 27 | 56.2 | 4 | US-09-036-987A-6 | Sequence 6, Appli |
| 554 | 27 | 56.2 | 515 | 4 | US-09-453-956-5 | Sequence 5, Appli | 627 | 27 | 56.2 | 3 | US-09-370-700-6 | Sequence 6, Appli |
| 555 | 27 | 56.2 | 519 | 1 | US-08-313-387-4 | Sequence 4, Appli | 628 | 27 | 56.2 | 3 | US-09-603-207-6 | Sequence 6, Appli |
| 556 | 27 | 56.2 | 549 | 4 | US-09-543-681A-4720 | Sequence 4720, Ap | 629 | 27 | 56.2 | 4 | US-09-902-540-15928 | Sequence 15928, A |
| 557 | 27 | 56.2 | 558 | 4 | US-09-770-517C-2 | Sequence 2, Appli | 630 | 26.5 | 55.2 | 4 | US-09-107-433-2798 | Sequence 2798, Ap |
| 558 | 27 | 56.2 | 565 | 4 | US-09-489-039A-13004 | Sequence 13004, A | 631 | 26.5 | 55.2 | 4 | US-09-270-767-42079 | Sequence 42079, A |
| 559 | 27 | 56.2 | 573 | 4 | US-09-134-000C-6366 | Sequence 6366, Ap | 632 | 26.5 | 55.2 | 4 | US-09-413-814-88 | Sequence 88, Appli |
| 560 | 27 | 56.2 | 576 | 4 | US-09-578-921A-2 | Sequence 2, Appli | 633 | 26.5 | 55.2 | 4 | US-09-321-987B-5 | Sequence 5, Appli |
| 561 | 27 | 56.2 | 581 | 4 | US-09-489-039A-10603 | Sequence 10603, A | 634 | 26.5 | 55.2 | 4 | US-09-491-523-5 | Sequence 5, Appli |
| 562 | 27 | 56.2 | 582 | 4 | US-09-543-681A-5938 | Sequence 5938, Ap | 635 | 26.5 | 55.2 | 4 | US-09-949-016-11401 | Sequence 11401, A |
| 563 | 27 | 56.2 | 599 | 4 | US-09-538-092-864 | Sequence 864, App | 636 | 26.5 | 55.2 | 4 | US-08-937-236-3 | Sequence 3, Appli |
| 564 | 27 | 56.2 | 605 | 3 | US-09-394-645-2 | Sequence 2, Appli | 637 | 26.5 | 55.2 | 3 | US-08-937-236-6 | Sequence 6, Appli |
| 565 | 27 | 56.2 | 615 | 4 | US-09-345-473E-49 | Sequence 49, Appli | 638 | 26.5 | 55.2 | 3 | US-08-569-214-3 | Sequence 3, Appli |
| 566 | 27 | 56.2 | 616 | 4 | US-08-637-670-26 | Sequence 26, Appli | 639 | 26.5 | 55.2 | 3 | US-08-937-236-2 | Sequence 2, Appli |
| 567 | 27 | 56.2 | 620 | 4 | US-08-637-670-28 | Sequence 28, Appli | 640 | 26.5 | 55.2 | 3 | US-08-569-214-5 | Sequence 5, Appli |
| 568 | 27 | 56.2 | 624 | 4 | US-09-637-670-40 | Sequence 40, Appli | 641 | 26.5 | 55.2 | 3 | US-08-569-214-6 | Sequence 6, Appli |
| 569 | 27 | 56.2 | 625 | 4 | US-09-902-540-12827 | Sequence 12827, A | 642 | 26.5 | 55.2 | 3 | US-08-937-236-5 | Sequence 5, Appli |
| 570 | 27 | 56.2 | 638 | 3 | US-09-347-488-2 | Sequence 2, Appli | 643 | 26.5 | 55.2 | 3 | US-08-569-214-2 | Sequence 2, Appli |
| 571 | 27 | 56.2 | 639 | 3 | US-09-376-856-2 | Sequence 2, Appli | 644 | 26.5 | 55.2 | 3 | US-09-328-352-5503 | Sequence 5503, Ap |
| 572 | 27 | 56.2 | 671 | 4 | US-09-328-352-6003 | Sequence 6003, Ap | 645 | 26.5 | 55.2 | 3 | US-09-181-336-9 | Sequence 9, Appli |
| 573 | 27 | 56.2 | 672 | 4 | US-09-336-115C-10 | Sequence 10, Appli | 646 | 26 | 54.2 | 12 | US-08-602-999A-221 | Sequence 221, App |
| 574 | 27 | 56.2 | 688 | 4 | US-09-949-016-11400 | Sequence 11400, A | 647 | 26 | 54.2 | 16 | US-09-500-124-221 | Sequence 221, App |
| 575 | 27 | 56.2 | 720 | 4 | US-09-394-272-14 | Sequence 14, Appli | 648 | 26 | 54.2 | 30 | US-09-690-454-116 | Sequence 116, App |
| 576 | 27 | 56.2 | 734 | 4 | US-09-726-219A-261 | Sequence 261, App | 649 | 26 | 54.2 | 51 | US-09-583-110-3296 | Sequence 3296, Ap |
| 577 | 27 | 56.2 | 740 | 4 | US-09-538-092-1178 | Sequence 1178, Ap | 650 | 26 | 54.2 | 66 | US-09-248-796A-22537 | Sequence 22537, A |
| 578 | 27 | 56.2 | 809 | 4 | US-09-543-681A-6686 | Sequence 6686, Ap | 651 | 26 | 54.2 | 66 | US-09-248-796A-27118 | Sequence 27118, A |
| 579 | 27 | 56.2 | 838 | 4 | US-09-252-991A-25809 | Sequence 25809, Ap | 652 | 26 | 54.2 | 67 | US-09-513-999C-6385 | Sequence 6385, Ap |
| 580 | 27 | 56.2 | 850 | 4 | US-09-902-540-12202 | Sequence 12202, A | 653 | 26 | 54.2 | 67 | US-09-911-927-33 | Sequence 33, Appli |
| 581 | 27 | 56.2 | 864 | 4 | US-09-134-000C-6025 | Sequence 6025, Ap | 654 | 26 | 54.2 | 68 | US-09-911-927-33 | Sequence 33, Appli |
| 582 | 27 | 56.2 | 898 | 3 | US-08-863-102-1 | Sequence 1, Appli | 655 | 26 | 54.2 | 68 | US-09-911-888-33 | Sequence 9, Appli |
| 583 | 27 | 56.2 | 907 | 3 | US-08-863-102-2 | Sequence 2, Appli | 656 | 26 | 54.2 | 69 | US-09-025-151-9 | Sequence 9, Appli |
| 584 | 27 | 56.2 | 911 | 4 | US-08-863-102-2 | Sequence 2, Appli | 657 | 26 | 54.2 | 69 | US-08-965-762-33 | Sequence 33, Appli |
| 585 | 27 | 56.2 | 914 | 4 | US-09-489-039A-13026 | Sequence 13026, A | 658 | 26 | 54.2 | 69 | US-09-637-240-9 | Sequence 9, Appli |
| 586 | 27 | 56.2 | 917 | 4 | US-08-259-451-11 | Sequence 11, Appli | 659 | 26 | 54.2 | 71 | US-08-840-767-44 | Sequence 44, Appli |
| 587 | 27 | 56.2 | 929 | 3 | US-09-328-352-4591 | Sequence 4591, Ap | 660 | 26 | 54.2 | 72 | US-09-543-681A-4438 | Sequence 4438, Ap |
| 588 | 27 | 56.2 | 950 | 3 | US-09-449-285A-4 | Sequence 4, Appli | 661 | 26 | 54.2 | 74 | US-09-543-681A-6642 | Sequence 6642, Ap |
| 589 | 27 | 56.2 | 955 | 4 | US-09-543-681A-6133 | Sequence 6133, Ap | 662 | 26 | 54.2 | 75 | US-08-905-223-277 | Sequence 277, App |
| 590 | 27 | 56.2 | 965 | 4 | US-09-437-277-3 | Sequence 3, Appli | 663 | 26 | 54.2 | 79 | US-09-198-452A-1191 | Sequence 1191, Ap |
| 591 | 27 | 56.2 | 972 | 3 | US-08-335-844A-24 | Sequence 24, Appli | 664 | 26 | 54.2 | 83 | US-09-621-976-4688 | Sequence 4688, Ap |
| 592 | 27 | 56.2 | 973 | 3 | US-09-129-366-24 | Sequence 24, Appli | 665 | 26 | 54.2 | 86 | US-09-621-976-4688 | Sequence 15589, A |
| 593 | 27 | 56.2 | 977 | 3 | US-08-335-844A-22 | Sequence 22, Appli | 666 | 26 | 54.2 | 90 | US-09-489-039A-11834 | Sequence 11834, A |
| 594 | 27 | 56.2 | 977 | 3 | US-09-129-366-22 | Sequence 22, Appli | 667 | 26 | 54.2 | 94 | US-09-513-999C-6216 | Sequence 6216, Ap |
| 595 | 27 | 56.2 | 977 | 4 | US-09-129-366-22 | Sequence 22, Appli | 668 | 26 | 54.2 | 98 | US-09-902-540-15680 | Sequence 15680, A |
| 596 | 27 | 56.2 | 987 | 4 | US-09-949-016-10265 | Sequence 10265, A | 669 | 26 | 54.2 | 100 | US-09-518-046-15 | Sequence 15, Appli |
| 597 | 27 | 56.2 | 1002 | 4 | US-09-762-724-4 | Sequence 4, Appli | 670 | 26 | 54.2 | 101 | US-09-518-046-15 | Sequence 15, Appli |
| 598 | 27 | 56.2 | 1032 | 3 | US-09-115-954-8 | Sequence 8, Appli | 671 | 26 | 54.2 | 101 | US-09-248-796A-19931 | Sequence 19931, A |
| 599 | 27 | 56.2 | 1044 | 3 | US-09-115-954-8 | Sequence 2, Appli | 672 | 26 | 54.2 | 101 | US-09-936-165A-440 | Sequence 440, App |
| 600 | 27 | 56.2 | 1063 | 4 | US-09-595-857B-29 | Sequence 29, Appli | 673 | 26 | 54.2 | 109 | US-09-673-395A-470 | Sequence 470, App |
| 601 | 27 | 56.2 | 1081 | 4 | US-09-529-239D-19 | Sequence 19, Appli | 674 | 26 | 54.2 | 109 | US-09-673-395A-486 | Sequence 486, App |
| 602 | 27 | 56.2 | 1085 | 4 | US-09-734-674-4 | Sequence 4, Appli | 675 | 26 | 54.2 | 109 | US-09-673-395A-622 | Sequence 622, App |
| 603 | 27 | 56.2 | 1157 | 4 | US-09-538-092-1328 | Sequence 1328, Ap | 676 | 26 | 54.2 | 109 | US-09-513-999C-8128 | Sequence 8128, Ap |
| 604 | 27 | 56.2 | 1225 | 4 | US-09-583-110-3637 | Sequence 3637, Ap | 677 | 26 | 54.2 | 112 | US-09-893-737-66 | Sequence 66, Appli |
| 605 | 27 | 56.2 | 1236 | 4 | US-09-883-134-4 | Sequence 4, Appli | 678 | 26 | 54.2 | 113 | US-09-489-039A-11952 | Sequence 11952, A |
| 606 | 27 | 56.2 | 1239 | 4 | US-09-107-433-4267 | Sequence 4267, Ap | 679 | 26 | 54.2 | 114 | US-09-513-999C-5733 | Sequence 5733, Ap |
| 607 | 27 | 56.2 | 1260 | 4 | US-09-328-352-6746 | Sequence 6746, Ap | 680 | 26 | 54.2 | 115 | US-08-516-859A-100 | Sequence 100, App |
| 608 | 27 | 56.2 | 1475 | 3 | US-09-538-092-1160 | Sequence 1160, Ap | 681 | 26 | 54.2 | 115 | US-09-586-472-100 | Sequence 100, App |
| 609 | 27 | 56.2 | 1618 | 3 | US-08-462-467B-4 | Sequence 4, Appli | 682 | 26 | 54.2 | 115 | US-09-528-706-100 | Sequence 100, App |
| 610 | 27 | 56.2 | 2008 | 4 | US-09-091-501B-8 | Sequence 8, Appli | 683 | 26 | 54.2 | 115 | US-09-270-767-44981 | Sequence 44981, A |
| 611 | 27 | 56.2 | 2325 | 3 | US-08-417-089-6 | Sequence 6, Appli | 684 | 26 | 54.2 | 115 | | |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|----------------------|--------------------|-----|----|------|-----|---|----------------------|--------------------|
| 685 | 26 | 54.2 | 118 | 4 | US-09-543-681A-5800 | Sequence 5800, Ap | 758 | 26 | 54.2 | 252 | 4 | US-09-543-681A-4245 | Sequence 4245, Ap |
| 686 | 26 | 54.2 | 119 | 1 | US-07-828-853-1 | Sequence 1, Appli | 759 | 26 | 54.2 | 254 | 4 | US-09-543-681A-7648 | Sequence 7648, Ap |
| 687 | 26 | 54.2 | 120 | 2 | US-08-937-972-5 | Sequence 5, Appli | 760 | 26 | 54.2 | 256 | 4 | US-09-134-001C-4116 | Sequence 4116, Ap |
| 688 | 26 | 54.2 | 126 | 4 | US-08-248-796A-15590 | Sequence 15590, A | 761 | 26 | 54.2 | 256 | 4 | US-09-902-540-13951 | Sequence 13951, A |
| 689 | 26 | 54.2 | 132 | 4 | US-09-732-210-1313 | Sequence 1313, Ap | 762 | 26 | 54.2 | 260 | 3 | US-09-134-001C-4872 | Sequence 4872, Ap |
| 690 | 26 | 54.2 | 132 | 4 | US-09-732-210-1314 | Sequence 1314, Ap | 763 | 26 | 54.2 | 260 | 4 | US-09-248-796A-17789 | Sequence 17789, A |
| 691 | 26 | 54.2 | 133 | 4 | US-09-270-767-57154 | Sequence 57154, A | 764 | 26 | 54.2 | 260 | 4 | US-09-248-796A-18584 | Sequence 18584, A |
| 692 | 26 | 54.2 | 134 | 4 | US-09-621-976-40311 | Sequence 40311, Ap | 765 | 26 | 54.2 | 264 | 4 | US-09-270-767-33115 | Sequence 33115, A |
| 693 | 26 | 54.2 | 138 | 4 | US-09-902-540-10829 | Sequence 10829, A | 766 | 26 | 54.2 | 264 | 4 | US-09-270-767-41787 | Sequence 41787, A |
| 694 | 26 | 54.2 | 139 | 4 | US-09-328-352-7201 | Sequence 7201, Ap | 767 | 26 | 54.2 | 264 | 4 | US-09-270-767-48332 | Sequence 48332, A |
| 695 | 26 | 54.2 | 142 | 4 | US-09-328-352-7201 | Sequence 7201, Ap | 768 | 26 | 54.2 | 264 | 4 | US-09-319-989-2 | Sequence 2, Appli |
| 696 | 26 | 54.2 | 143 | 4 | US-09-134-000C-4059 | Sequence 4059, Ap | 769 | 26 | 54.2 | 265 | 3 | US-09-328-352-4811 | Sequence 4811, Ap |
| 697 | 26 | 54.2 | 144 | 4 | US-09-230-078A-6 | Sequence 6, Appli | 770 | 26 | 54.2 | 265 | 4 | US-09-248-796A-16392 | Sequence 16392, A |
| 698 | 26 | 54.2 | 144 | 4 | US-09-902-540-12977 | Sequence 12977, A | 771 | 26 | 54.2 | 265 | 4 | US-09-538-092-325 | Sequence 325, App |
| 699 | 26 | 54.2 | 145 | 4 | US-09-270-767-47454 | Sequence 47454, A | 772 | 26 | 54.2 | 266 | 4 | US-09-134-000C-4815 | Sequence 4815, Ap |
| 700 | 26 | 54.2 | 146 | 4 | US-09-270-767-32237 | Sequence 32237, A | 773 | 26 | 54.2 | 267 | 4 | US-09-602-777A-156 | Sequence 156, App |
| 701 | 26 | 54.2 | 148 | 4 | US-09-252-991A-18029 | Sequence 18029, A | 774 | 26 | 54.2 | 267 | 4 | US-09-602-777A-158 | Sequence 158, App |
| 702 | 26 | 54.2 | 151 | 4 | US-09-902-540-10111 | Sequence 10111, A | 775 | 26 | 54.2 | 269 | 3 | US-09-134-001C-3461 | Sequence 3461, Ap |
| 703 | 26 | 54.2 | 155 | 4 | US-09-270-767-32485 | Sequence 32485, A | 776 | 26 | 54.2 | 273 | 4 | US-09-270-767-60531 | Sequence 60531, A |
| 704 | 26 | 54.2 | 155 | 4 | US-09-270-767-47702 | Sequence 47702, A | 777 | 26 | 54.2 | 277 | 4 | US-09-252-991A-29257 | Sequence 29257, A |
| 705 | 26 | 54.2 | 159 | 3 | US-08-796-792-2 | Sequence 2, Appli | 778 | 26 | 54.2 | 277 | 4 | US-09-198-452A-555 | Sequence 555, App |
| 706 | 26 | 54.2 | 159 | 4 | US-09-198-452A-462 | Sequence 462, App | 779 | 26 | 54.2 | 277 | 4 | US-09-438-185A-516 | Sequence 516, App |
| 707 | 26 | 54.2 | 159 | 4 | US-09-491-795-2 | Sequence 2, Appli | 780 | 26 | 54.2 | 278 | 4 | US-09-792-024-100 | Sequence 100, App |
| 708 | 26 | 54.2 | 160 | 4 | US-09-252-991A-31843 | Sequence 31843, A | 781 | 26 | 54.2 | 278 | 4 | US-09-902-540-16068 | Sequence 16068, A |
| 709 | 26 | 54.2 | 160 | 4 | US-09-270-767-42694 | Sequence 42694, A | 782 | 26 | 54.2 | 279 | 4 | US-09-134-000C-6430 | Sequence 6430, Ap |
| 710 | 26 | 54.2 | 165 | 1 | US-08-233-788A-40 | Sequence 40, Appl | 783 | 26 | 54.2 | 279 | 4 | US-09-270-767-35048 | Sequence 35048, A |
| 711 | 26 | 54.2 | 165 | 1 | US-09-252-991A-27037 | Sequence 27037, A | 784 | 26 | 54.2 | 279 | 4 | US-09-270-767-50285 | Sequence 50285, A |
| 712 | 26 | 54.2 | 166 | 4 | US-09-248-796A-14783 | Sequence 14783, A | 785 | 26 | 54.2 | 279 | 4 | US-09-710-279-858 | Sequence 858, App |
| 713 | 26 | 54.2 | 167 | 4 | US-09-902-540-13832 | Sequence 13832, A | 786 | 26 | 54.2 | 279 | 4 | US-09-925-637-50 | Sequence 50, Appl |
| 714 | 26 | 54.2 | 170 | 3 | US-08-858-207A-519 | Sequence 519, App | 787 | 26 | 54.2 | 281 | 4 | US-09-248-796A-17769 | Sequence 17769, A |
| 715 | 26 | 54.2 | 172 | 4 | US-09-252-991A-26790 | Sequence 26790, A | 788 | 26 | 54.2 | 282 | 4 | US-09-270-767-43326 | Sequence 43326, A |
| 716 | 26 | 54.2 | 173 | 4 | US-09-902-540-11877 | Sequence 11877, A | 789 | 26 | 54.2 | 284 | 3 | US-09-134-001C-3329 | Sequence 3329, Ap |
| 717 | 26 | 54.2 | 175 | 4 | US-09-902-540-16269 | Sequence 16269, A | 790 | 26 | 54.2 | 284 | 3 | US-09-489-039A-13043 | Sequence 13043, A |
| 718 | 26 | 54.2 | 176 | 1 | US-08-449-922-1 | Sequence 1, Appli | 791 | 26 | 54.2 | 285 | 4 | US-09-248-796A-15972 | Sequence 15972, A |
| 719 | 26 | 54.2 | 178 | 4 | US-09-270-767-36123 | Sequence 36123, A | 792 | 26 | 54.2 | 287 | 4 | US-09-252-991A-22466 | Sequence 22466, A |
| 720 | 26 | 54.2 | 178 | 4 | US-09-270-767-51340 | Sequence 51340, A | 793 | 26 | 54.2 | 289 | 4 | US-09-248-796A-19772 | Sequence 19772, A |
| 721 | 26 | 54.2 | 180 | 4 | US-09-230-078A-4 | Sequence 4, Appli | 794 | 26 | 54.2 | 293 | 4 | US-09-489-039A-7890 | Sequence 7890, Ap |
| 722 | 26 | 54.2 | 183 | 4 | US-09-107-532A-4014 | Sequence 4014, Ap | 795 | 26 | 54.2 | 297 | 4 | US-09-543-681A-8242 | Sequence 8242, Ap |
| 723 | 26 | 54.2 | 183 | 4 | US-09-107-532A-5935 | Sequence 5935, Ap | 796 | 26 | 54.2 | 297 | 4 | US-09-107-433-5074 | Sequence 5074, Ap |
| 724 | 26 | 54.2 | 186 | 4 | US-09-248-796A-26092 | Sequence 26092, A | 797 | 26 | 54.2 | 298 | 4 | US-09-270-767-45154 | Sequence 45154, A |
| 725 | 26 | 54.2 | 187 | 4 | US-09-242-890-1 | Sequence 1, Appli | 798 | 26 | 54.2 | 299 | 4 | US-09-949-016-8018 | Sequence 8018, Ap |
| 726 | 26 | 54.2 | 190 | 4 | US-09-270-767-43995 | Sequence 43995, A | 799 | 26 | 54.2 | 302 | 4 | US-09-270-767-59138 | Sequence 59138, Ap |
| 727 | 26 | 54.2 | 191 | 4 | US-09-248-796A-20248 | Sequence 20248, A | 800 | 26 | 54.2 | 303 | 4 | US-09-252-991A-27866 | Sequence 27866, A |
| 728 | 26 | 54.2 | 194 | 4 | US-09-248-796A-14593 | Sequence 14593, A | 801 | 26 | 54.2 | 303 | 4 | US-09-902-540-11322 | Sequence 11322, A |
| 729 | 26 | 54.2 | 199 | 2 | US-08-831-575-8 | Sequence 8, Appli | 802 | 26 | 54.2 | 303 | 4 | US-09-302-540-14454 | Sequence 14454, A |
| 730 | 26 | 54.2 | 199 | 2 | US-08-831-575-9 | Sequence 9, Appli | 803 | 26 | 54.2 | 304 | 4 | US-09-538-092-155 | Sequence 155, App |
| 731 | 26 | 54.2 | 199 | 4 | US-09-710-279-1342 | Sequence 1342, Ap | 804 | 26 | 54.2 | 307 | 4 | US-09-543-681A-18385 | Sequence 18385, A |
| 732 | 26 | 54.2 | 200 | 4 | US-09-489-039A-11359 | Sequence 11359, A | 805 | 26 | 54.2 | 309 | 4 | US-09-252-991A-19385 | Sequence 19385, A |
| 733 | 26 | 54.2 | 200 | 4 | US-09-242-890-10 | Sequence 10, Appl | 806 | 26 | 54.2 | 309 | 4 | US-09-603-208A-110 | Sequence 110, App |
| 734 | 26 | 54.2 | 203 | 4 | US-09-252-991A-21364 | Sequence 21364, A | 807 | 26 | 54.2 | 310 | 1 | US-08-433-783-42 | Sequence 42, Appl |
| 735 | 26 | 54.2 | 204 | 4 | US-09-902-540-14744 | Sequence 14744, A | 808 | 26 | 54.2 | 310 | 1 | US-08-337-358-42 | Sequence 42, Appl |
| 736 | 26 | 54.2 | 208 | 2 | US-08-606-143-41 | Sequence 41, Appl | 809 | 26 | 54.2 | 310 | 4 | US-09-270-767-47942 | Sequence 47942, A |
| 737 | 26 | 54.2 | 208 | 2 | US-08-606-143-43 | Sequence 43, Appl | 810 | 26 | 54.2 | 310 | 5 | PCT-US95-07537A-42 | Sequence 42, Appl |
| 738 | 26 | 54.2 | 213 | 4 | US-09-107-532A-3797 | Sequence 3797, Ap | 811 | 26 | 54.2 | 310 | 5 | PCT-US95-07537-42 | Sequence 42, Appl |
| 739 | 26 | 54.2 | 213 | 4 | US-09-270-767-56727 | Sequence 56727, A | 812 | 26 | 54.2 | 311 | 4 | US-09-583-110-2874 | Sequence 2874, Ap |
| 740 | 26 | 54.2 | 217 | 4 | US-09-650-454-112 | Sequence 112, App | 813 | 26 | 54.2 | 313 | 3 | US-09-336-643A-81 | Sequence 81, Appl |
| 741 | 26 | 54.2 | 219 | 4 | US-09-484-577A-32 | Sequence 32, Appl | 814 | 26 | 54.2 | 313 | 4 | US-09-561-763-8 | Sequence 8, Appli |
| 742 | 26 | 54.2 | 220 | 4 | US-09-252-991A-16651 | Sequence 16651, A | 815 | 26 | 54.2 | 313 | 4 | US-09-431-367B-8 | Sequence 8, Appli |
| 743 | 26 | 54.2 | 224 | 4 | US-09-229-583A-2 | Sequence 2, Appli | 816 | 26 | 54.2 | 315 | 4 | US-09-248-796A-19532 | Sequence 19532, A |
| 744 | 26 | 54.2 | 224 | 4 | US-09-242-890-11 | Sequence 11, Appl | 817 | 26 | 54.2 | 317 | 2 | US-08-864-799-5 | Sequence 5, Appli |
| 745 | 26 | 54.2 | 224 | 4 | US-10-187-904-2 | Sequence 2, Appli | 818 | 26 | 54.2 | 317 | 2 | US-09-949-016-11333 | Sequence 11333, A |
| 746 | 26 | 54.2 | 224 | 4 | US-09-248-796A-14183 | Sequence 14183, A | 819 | 26 | 54.2 | 318 | 1 | US-08-599-480-2 | Sequence 2, Appli |
| 747 | 26 | 54.2 | 224 | 4 | US-09-248-796A-15240 | Sequence 15240, A | 820 | 26 | 54.2 | 318 | 2 | US-08-842-199-2 | Sequence 2, Appli |
| 748 | 26 | 54.2 | 226 | 4 | US-09-248-796A-20804 | Sequence 20804, A | 821 | 26 | 54.2 | 318 | 4 | US-09-172-070-2 | Sequence 2, Appli |
| 749 | 26 | 54.2 | 235 | 4 | US-09-252-991A-29814 | Sequence 29814, A | 822 | 26 | 54.2 | 318 | 5 | PCT-US95-00190-2 | Sequence 2, Appli |
| 750 | 26 | 54.2 | 243 | 4 | US-09-489-039A-13870 | Sequence 13870, A | 823 | 26 | 54.2 | 320 | 4 | US-09-526-400-2 | Sequence 2, Appli |
| 751 | 26 | 54.2 | 244 | 4 | US-09-710-279-566 | Sequence 566, App | 824 | 26 | 54.2 | 322 | 4 | US-09-724-797-56 | Sequence 56, Appl |
| 752 | 26 | 54.2 | 246 | 3 | US-09-134-001C-5292 | Sequence 5292, Ap | 825 | 26 | 54.2 | 323 | 4 | US-09-438-185A-443 | Sequence 443, App |
| 753 | 26 | 54.2 | 247 | 4 | US-09-248-796A-14828 | Sequence 14828, Ap | 826 | 26 | 54.2 | 323 | 4 | US-09-134-000C-4346 | Sequence 4346, Ap |
| 754 | 26 | 54.2 | 249 | 4 | US-09-270-767-38338 | Sequence 38338, A | 827 | 26 | 54.2 | 328 | 4 | US-09-270-767-59817 | Sequence 59817, A |
| 755 | 26 | 54.2 | 249 | 4 | US-09-270-767-53555 | Sequence 53555, A | 828 | 26 | 54.2 | 335 | 4 | US-09-252-991A-22013 | Sequence 22013, A |
| 756 | 26 | 54.2 | 251 | 4 | US-09-710-279-3050 | Sequence 3050, Ap | 829 | 26 | 54.2 | 336 | 4 | US-09-248-796A-17499 | Sequence 17499, A |
| 757 | 26 | 54.2 | 251 | 4 | US-10-000-489-26 | Sequence 26, Appl | 830 | 26 | 54.2 | 336 | 4 | US-09-949-016-7218 | Sequence 7218, Ap |

| | | | | | | | | | | | | | |
|-----|----|------|-----|---|----------------------|--------------------|-----|----|------|-----|---|----------------------|--------------------|
| 831 | 26 | 54.2 | 337 | 4 | US-09-583-110-3391 | Sequence 3391, Ap | 904 | 26 | 54.2 | 433 | 4 | US-09-949-016-7709 | Sequence 7709, Ap |
| 832 | 26 | 54.2 | 338 | 1 | US-08-891-254-1 | Sequence 1, Appli | 905 | 26 | 54.2 | 434 | 4 | US-09-949-016-7735 | Sequence 7735, Ap |
| 833 | 26 | 54.2 | 338 | 2 | US-08-484-358-2 | Sequence 2, Appli | 906 | 26 | 54.2 | 436 | 4 | US-09-252-991A-18821 | Sequence 18821, A |
| 834 | 26 | 54.2 | 338 | 2 | US-08-819-539-1 | Sequence 1, Appli | 907 | 26 | 54.2 | 445 | 3 | US-08-974-691-6 | Sequence 6, Appli |
| 835 | 26 | 54.2 | 338 | 2 | US-09-030-270A-1 | Sequence 2, Appli | 908 | 26 | 54.2 | 451 | 1 | US-08-154-365-2 | Sequence 2, Appli |
| 836 | 26 | 54.2 | 338 | 3 | US-09-118-959-2 | Sequence 2, Appli | 909 | 26 | 54.2 | 451 | 1 | US-08-453-117-2 | Sequence 2, Appli |
| 837 | 26 | 54.2 | 338 | 3 | US-08-984-207-1 | Sequence 1, Appli | 910 | 26 | 54.2 | 451 | 2 | US-08-948-222-2 | Sequence 2, Appli |
| 838 | 26 | 54.2 | 338 | 3 | US-09-013-587-1 | Sequence 1, Appli | 911 | 26 | 54.2 | 451 | 2 | US-08-973-145-2 | Sequence 10, Appli |
| 839 | 26 | 54.2 | 338 | 3 | US-09-086-118-21 | Sequence 21, Appli | 912 | 26 | 54.2 | 451 | 3 | US-09-276-400-10 | Sequence 10, Appli |
| 840 | 26 | 54.2 | 338 | 4 | US-09-431-614-1 | Sequence 1, Appli | 913 | 26 | 54.2 | 451 | 3 | US-08-974-691-2 | Sequence 10, Appli |
| 841 | 26 | 54.2 | 338 | 5 | PCT-US96-08819-1 | Sequence 1, Appli | 914 | 26 | 54.2 | 451 | 3 | US-09-448-076-10 | Sequence 10, Appli |
| 842 | 26 | 54.2 | 340 | 1 | US-07-828-700-8 | Sequence 8, Appli | 915 | 26 | 54.2 | 451 | 3 | US-09-702-572-10 | Sequence 10, Appli |
| 843 | 26 | 54.2 | 340 | 3 | US-09-360-779-2 | Sequence 2, Appli | 916 | 26 | 54.2 | 451 | 3 | US-09-270-767-45139 | Sequence 2, Appli |
| 844 | 26 | 54.2 | 340 | 3 | US-09-435-335-2 | Sequence 2, Appli | 917 | 26 | 54.2 | 451 | 5 | PCT-US96-08081-2 | Sequence 2, Appli |
| 845 | 26 | 54.2 | 343 | 4 | US-09-328-352-6577 | Sequence 6577, Ap | 918 | 26 | 54.2 | 453 | 6 | 5510466-4 | Patent No. 5510466 |
| 846 | 26 | 54.2 | 344 | 4 | US-09-724-623-79 | Sequence 79, Appli | 919 | 26 | 54.2 | 453 | 6 | 5510466-4 | Patent No. 5510466 |
| 847 | 26 | 54.2 | 345 | 4 | US-09-214-631-5 | Sequence 5, Appli | 920 | 26 | 54.2 | 453 | 6 | 5510466-4 | Patent No. 5510466 |
| 848 | 26 | 54.2 | 346 | 1 | US-08-213-403-2 | Sequence 2, Appli | 921 | 26 | 54.2 | 454 | 4 | US-09-240-639-11 | Sequence 11, Appli |
| 849 | 26 | 54.2 | 346 | 1 | US-08-458-077-2 | Sequence 2, Appli | 922 | 26 | 54.2 | 454 | 4 | US-09-538-092-1156 | Sequence 11, Appli |
| 850 | 26 | 54.2 | 346 | 1 | US-08-460-741-2 | Sequence 2, Appli | 923 | 26 | 54.2 | 454 | 4 | US-09-908-510A-11 | Sequence 11, Appli |
| 851 | 26 | 54.2 | 346 | 1 | US-08-747-240-2 | Sequence 2, Appli | 924 | 26 | 54.2 | 454 | 4 | US-09-905-744B-11 | Sequence 11, Appli |
| 852 | 26 | 54.2 | 346 | 1 | US-08-299-567-6 | Sequence 6, Appli | 925 | 26 | 54.2 | 454 | 4 | US-10-107-660-11 | Sequence 11, Appli |
| 853 | 26 | 54.2 | 346 | 4 | US-09-039-642B-2 | Sequence 2, Appli | 926 | 26 | 54.2 | 454 | 4 | US-09-107-576-11 | Sequence 11, Appli |
| 854 | 26 | 54.2 | 346 | 4 | US-08-635-130A-9 | Sequence 9, Appli | 927 | 26 | 54.2 | 454 | 4 | US-09-905-732B-11 | Sequence 11, Appli |
| 855 | 26 | 54.2 | 347 | 4 | US-09-949-016-9849 | Sequence 9849, Ap | 928 | 26 | 54.2 | 456 | 4 | US-09-134-000C-6463 | Sequence 6463, Ap |
| 856 | 26 | 54.2 | 347 | 4 | US-08-462-467B-18 | Sequence 18, Appli | 929 | 26 | 54.2 | 456 | 4 | US-09-248-796A-17048 | Sequence 17048, A |
| 857 | 26 | 54.2 | 352 | 1 | US-08-482-577B-18 | Sequence 2, Appli | 930 | 26 | 54.2 | 462 | 4 | US-09-976-594-427 | Sequence 427, Ap |
| 858 | 26 | 54.2 | 352 | 3 | US-08-289-222E-4 | Sequence 4, Appli | 931 | 26 | 54.2 | 469 | 1 | US-08-313-288B-15 | Sequence 15, Appli |
| 859 | 26 | 54.2 | 352 | 3 | US-09-218-176-2 | Sequence 2, Appli | 932 | 26 | 54.2 | 470 | 4 | US-09-896-319A-35 | Sequence 35, Appli |
| 860 | 26 | 54.2 | 352 | 3 | US-09-054-526B-4 | Sequence 4, Appli | 933 | 26 | 54.2 | 473 | 3 | US-08-914-375C-71 | Sequence 71, Appli |
| 861 | 26 | 54.2 | 352 | 4 | US-08-981-490B-3 | Sequence 3, Appli | 934 | 26 | 54.2 | 476 | 4 | US-09-107-532A-5076 | Sequence 5076, Ap |
| 862 | 26 | 54.2 | 354 | 3 | US-09-134-001C-5588 | Sequence 5588, Ap | 935 | 26 | 54.2 | 477 | 1 | US-07-791-936A-2 | Sequence 2, Appli |
| 863 | 26 | 54.2 | 354 | 4 | US-09-107-433-3389 | Sequence 3389, Ap | 936 | 26 | 54.2 | 477 | 1 | US-08-383-781B-2 | Sequence 2, Appli |
| 864 | 26 | 54.2 | 356 | 4 | US-09-949-016-10384 | Sequence 10384, A | 937 | 26 | 54.2 | 477 | 4 | US-09-168-510-2 | Sequence 2, Appli |
| 865 | 26 | 54.2 | 363 | 4 | US-09-248-796A-15286 | Sequence 15286, A | 938 | 26 | 54.2 | 477 | 4 | US-09-826-509-493 | Sequence 493, Ap |
| 866 | 26 | 54.2 | 365 | 4 | US-09-134-000C-4369 | Sequence 4369, Ap | 939 | 26 | 54.2 | 478 | 4 | US-09-107-532A-6090 | Sequence 6090, Ap |
| 867 | 26 | 54.2 | 368 | 4 | US-09-252-991A-33020 | Sequence 33020, A | 940 | 26 | 54.2 | 478 | 4 | US-09-543-681A-7331 | Sequence 7331, A |
| 868 | 26 | 54.2 | 369 | 4 | US-09-252-991A-20245 | Sequence 20245, A | 941 | 26 | 54.2 | 479 | 4 | US-09-252-991A-24951 | Sequence 24951, A |
| 869 | 26 | 54.2 | 369 | 4 | US-10-138-701-36 | Sequence 36, Appli | 942 | 26 | 54.2 | 480 | 4 | US-09-538-092-200 | Sequence 200, Ap |
| 870 | 26 | 54.2 | 369 | 4 | US-09-902-540-12050 | Sequence 12050, A | 943 | 26 | 54.2 | 482 | 4 | US-09-949-016-9698 | Sequence 9698, Ap |
| 871 | 26 | 54.2 | 370 | 4 | US-09-252-991A-23998 | Sequence 23998, A | 944 | 26 | 54.2 | 484 | 4 | US-08-294-770A-2 | Sequence 2, Appli |
| 872 | 26 | 54.2 | 371 | 3 | US-09-043-627-10 | Sequence 10, Appli | 945 | 26 | 54.2 | 490 | 1 | US-08-448-735C-2 | Sequence 2, Appli |
| 873 | 26 | 54.2 | 376 | 4 | US-09-270-767-42614 | Sequence 42614, A | 946 | 26 | 54.2 | 491 | 2 | US-09-902-540-13995 | Sequence 13995, A |
| 874 | 26 | 54.2 | 386 | 4 | US-09-489-039A-8324 | Sequence 8324, Ap | 947 | 26 | 54.2 | 491 | 4 | US-09-902-540-11934 | Sequence 11934, A |
| 875 | 26 | 54.2 | 391 | 4 | US-09-270-767-44694 | Sequence 44694, A | 948 | 26 | 54.2 | 493 | 4 | US-09-134-000C-4549 | Sequence 4549, Ap |
| 876 | 26 | 54.2 | 392 | 4 | US-09-489-039A-9827 | Sequence 9827, Ap | 949 | 26 | 54.2 | 497 | 4 | US-09-328-352-5415 | Sequence 5415, Ap |
| 877 | 26 | 54.2 | 392 | 4 | US-09-902-540-12860 | Sequence 12860, A | 950 | 26 | 54.2 | 499 | 4 | US-09-270-767-43743 | Sequence 43743, A |
| 878 | 26 | 54.2 | 395 | 1 | US-08-723-938-3 | Sequence 3, Appli | 951 | 26 | 54.2 | 501 | 4 | US-09-252-991A-23445 | Sequence 23445, A |
| 879 | 26 | 54.2 | 395 | 2 | US-09-080-538-3 | Sequence 3, Appli | 952 | 26 | 54.2 | 509 | 4 | US-09-065-383-27 | Sequence 27, Appli |
| 880 | 26 | 54.2 | 395 | 4 | US-09-387-413-3 | Sequence 3, Appli | 953 | 26 | 54.2 | 518 | 3 | US-09-949-016-11189 | Sequence 11189, A |
| 881 | 26 | 54.2 | 398 | 4 | US-09-252-991A-21686 | Sequence 21686, A | 954 | 26 | 54.2 | 522 | 4 | US-08-246-583-3 | Sequence 3, Appli |
| 882 | 26 | 54.2 | 400 | 4 | US-09-691-270A-14 | Sequence 14, Appli | 955 | 26 | 54.2 | 542 | 1 | US-08-636-791A-5 | Sequence 5, Appli |
| 883 | 26 | 54.2 | 402 | 4 | US-09-252-991A-17143 | Sequence 17143, A | 956 | 26 | 54.2 | 542 | 4 | US-09-538-092-672 | Sequence 672, Ap |
| 884 | 26 | 54.2 | 409 | 1 | US-08-403-545-2 | Sequence 2, Appli | 957 | 26 | 54.2 | 542 | 4 | US-08-083-948-8 | Sequence 8, Appli |
| 885 | 26 | 54.2 | 409 | 3 | US-08-404-381-2 | Sequence 2, Appli | 958 | 26 | 54.2 | 547 | 1 | US-08-393-785-8 | Sequence 8, Appli |
| 886 | 26 | 54.2 | 412 | 4 | US-09-538-092-709 | Sequence 709, App | 959 | 26 | 54.2 | 547 | 1 | US-08-475-694-8 | Sequence 8, Appli |
| 887 | 26 | 54.2 | 414 | 4 | US-09-543-681A-6647 | Sequence 6647, Ap | 960 | 26 | 54.2 | 547 | 1 | US-08-713-057-8 | Sequence 36, Appli |
| 888 | 26 | 54.2 | 415 | 4 | US-09-538-092-708 | Sequence 708, App | 961 | 26 | 54.2 | 547 | 3 | US-09-347-878-36 | Sequence 13, Appli |
| 889 | 26 | 54.2 | 416 | 4 | US-09-538-092-708 | Sequence 708, App | 962 | 26 | 54.2 | 547 | 3 | US-08-630-172-13 | Sequence 13, Appli |
| 890 | 26 | 54.2 | 417 | 3 | US-08-462-467B-6 | Sequence 6, Appli | 963 | 26 | 54.2 | 553 | 3 | US-09-375-419-13 | Sequence 14, Appli |
| 891 | 26 | 54.2 | 417 | 3 | US-08-462-467B-10 | Sequence 10, Appli | 964 | 26 | 54.2 | 553 | 3 | US-09-465-559-14 | Sequence 14, Appli |
| 892 | 26 | 54.2 | 417 | 4 | US-09-248-796A-16038 | Sequence 16038, A | 965 | 26 | 54.2 | 553 | 4 | US-09-902-540-15181 | Sequence 22, Appli |
| 893 | 26 | 54.2 | 419 | 3 | US-09-064-411A-7 | Sequence 7, Appli | 966 | 26 | 54.2 | 554 | 3 | US-09-538-092-672 | Sequence 24, Appli |
| 894 | 26 | 54.2 | 420 | 3 | US-09-008-271A-4 | Sequence 4, Appli | 967 | 26 | 54.2 | 554 | 4 | US-08-462-467B-26 | Sequence 26, Appli |
| 895 | 26 | 54.2 | 420 | 3 | US-08-974-691-8 | Sequence 8, Appli | 968 | 26 | 54.2 | 556 | 3 | US-08-462-467B-26 | Sequence 12461, A |
| 896 | 26 | 54.2 | 420 | 4 | US-09-705-448-1 | Sequence 1, Appli | 969 | 26 | 54.2 | 556 | 3 | US-08-462-467B-26 | Sequence 17202, A |
| 897 | 26 | 54.2 | 421 | 4 | US-09-902-540-10569 | Sequence 10569, A | 970 | 26 | 54.2 | 556 | 4 | US-09-252-991A-17202 | Sequence 9311, Ap |
| 898 | 26 | 54.2 | 421 | 4 | US-09-248-796A-17203 | Sequence 17203, A | 971 | 26 | 54.2 | 558 | 4 | US-09-489-039A-9311 | Sequence 2, Appli |
| 899 | 26 | 54.2 | 428 | 3 | US-09-134-001C-4879 | Sequence 4879, Ap | 972 | 26 | 54.2 | 561 | 2 | US-08-532-795-2 | Sequence 41, Appli |
| 900 | 26 | 54.2 | 430 | 4 | US-09-248-796A-16772 | Sequence 22, Appli | 973 | 26 | 54.2 | 562 | 2 | US-08-484-993B-41 | Sequence 41, Appli |
| 901 | 26 | 54.2 | 433 | 3 | US-09-697-367-22 | Sequence 3, Appli | 974 | 26 | 54.2 | 566 | 2 | US-08-484-993B-41 | Sequence 41, Appli |
| 902 | 26 | 54.2 | 433 | 4 | US-09-705-448-3 | Sequence 3, Appli | 975 | 26 | 54.2 | 566 | 2 | US-08-484-993B-41 | Sequence 41, Appli |
| 903 | 26 | 54.2 | 433 | 4 | US-09-918-909A-22 | Sequence 22, Appli | 976 | 26 | 54.2 | 566 | 2 | US-08-484-993B-41 | Sequence 41, Appli |

```

977 26 54.2 566 2 US-08-484-596A-41 Sequence 41, Appl
978 26 54.2 566 2 US-08-480-150A-41 Sequence 41, Appl
979 26 54.2 566 3 US-08-458-731-41 Sequence 41, Appl
980 26 54.2 566 3 US-08-149-223A-41 Sequence 20411, A
981 26 54.2 566 4 US-09-248-796A-20411 Sequence 23, Appl
982 26 54.2 569 2 US-08-532-795-23 Sequence 29, Appl
983 26 54.2 569 2 US-08-532-795-29 Sequence 19, Appl
984 26 54.2 570 2 US-08-532-795-25 Sequence 21, Appl
985 26 54.2 571 2 US-08-532-795-19 Sequence 21, Appl
986 26 54.2 571 2 US-08-532-795-21 Sequence 27, Appl
987 26 54.2 574 2 US-08-532-795-27 Sequence 15452, A
988 26 54.2 577 4 US-09-902-540-15452 Sequence 15872, A
989 26 54.2 577 4 US-09-902-540-15872 Sequence 4, Appl
990 26 54.2 583 2 US-08-616-392C-4 Sequence 90, Appl
991 26 54.2 592 4 US-09-614-912-90 Sequence 18837, A
992 26 54.2 605 4 US-09-252-991A-18837 Sequence 4, Appl
993 26 54.2 613 4 US-09-949-016-9601 Sequence 4, Appl
994 26 54.2 614 1 US-08-262-338A-4 Sequence 38, Appl
995 26 54.2 614 1 US-08-460-114A-4 Sequence 10, Appl
996 26 54.2 614 3 US-09-347-878-38 Sequence 10, Appl
997 26 54.2 614 4 US-09-133-966A-4 Sequence 10, Appl
998 26 54.2 618 1 US-08-468-853-10 Sequence 10, Appl
999 26 54.2 618 1 US-08-468-855-10 Sequence 10, Appl
1000 26 54.2 618 1 US-08-310-357-10

```

ALIGNMENTS

```

RESULT 1
US-09-346-860-9
; Sequence 9, Application US/09346860
; Patent No. 6221641
; GENERAL INFORMATION:
; APPLICANT: Khosla, Chaitan
; APPLICANT: Lau, Janice
; APPLICANT: Pohl, Nicola L.
; TITLE OF INVENTION: METHOD FOR MAKING POLYKETIDES
; FILE REFERENCE: 30662-20025.00
; CURRENT APPLICATION NUMBER: US/09/346,860
; CURRENT FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Streptomyces sp.
US-09-346-860-9

```

```

Query Match 75.0%; Score 36; DB 3; Length 50;
Best Local Similarity 66.7%; Pred. No. 2.6;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 GPHETITAL 9
Db 5 GPHPTLTTL 13

```

```

RESULT 2
US-09-735-685-9
; Sequence 9, Application US/09735685
; Patent No. 6551802
; GENERAL INFORMATION:
; APPLICANT: Khosla, Chaitan
; APPLICANT: Lau, Janice
; APPLICANT: Pohl, Nicola L.
; TITLE OF INVENTION: METHOD FOR MAKING POLYKETIDES
; FILE REFERENCE: 30662-20025.00
; CURRENT APPLICATION NUMBER: US/09/735,685
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: US/09/346,860
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 15

```

```

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Streptomyces sp.
US-09-735-685-9

```

```

Query Match 75.0%; Score 36; DB 4; Length 50;
Best Local Similarity 66.7%; Pred. No. 2.6;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 GPHETITAL 9
Db 5 GPHPTLTTL 13

```

```

RESULT 3
US-08-905-223-493
; Sequence 493, Application US/08905223
; Patent No. 6222029
; GENERAL INFORMATION:
; APPLICANT: Edwards, Jean-Baptiste D.
; APPLICANT: Duelett, Aymeric
; APPLICANT: Lacroix, Bruno
; TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS
; NUMBER OF SEQUENCES: 503
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 501 West Broadway
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92101-3505
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Win95
; SOFTWARE: Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/905,223
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned A.
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 493:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 79 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PROTEIN
; ORIGINAL SOURCE:
; ORGANISM: Homo Sapiens
; TISSUE TYPE: Brain
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: -18...-1
; IDENTIFICATION METHOD: Von Heijne matrix
; OTHER INFORMATION: score 3.8
; OTHER INFORMATION: seq GXALGLPLSLAKA/ED
US-08-905-223-493

```

```

Query Match 75.0%; Score 36; DB 3; Length 79;
Best Local Similarity 66.7%; Pred. No. 4.5;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

QY 1 GPHETITAL 9
Db 54 GPHETLXL 62

```

```
RESULT 4
US-10-127-641-5
; Sequence 5, Application US/10127641
; Patent No. 6824778
; GENERAL INFORMATION:
; APPLICANT: Hart, Mary Kate
; TITLE OF INVENTION: Prophylactic and Therapeutic Monoclonal Antibodies
; FILE REFERENCE: 003/251/SAP
; CURRENT APPLICATION NUMBER: US/10/127,641
; CURRENT FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: US 60/285,601
; PRIOR FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 5
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Eastern equine encephalitis virus
US-10-127-641-5
Query Match 72.9%; Score 35; DB 4; Length 58;
Best Local Similarity 75.0%; Pred. No. 5;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PHETITAL 9
| | | | |
Db 30 PHETLTM 37

RESULT 5
US-03-248-796A-19847
; Sequence 19847, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19847
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Candida albicans
US-03-248-796A-19847
Query Match 72.9%; Score 35; DB 4; Length 91;
Best Local Similarity 87.5%; Pred. No. 8.4;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PHETITAL 9
| | | | |
Db 62 PHEVITAL 69

RESULT 6
US-08-997-080-154
; Sequence 154, Application US/08997080
; Patent No. 5968524
; GENERAL INFORMATION:
; APPLICANT: WATSON, JAMES D.
; APPLICANT: TAN, PAUL L.J.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR THE TREATMENT OF IMMUNOLOGICALLY-
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
```

```
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,080
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Sleath, Janet
REGISTRATION NUMBER: 37,007
REFERENCE/DOCKET NUMBER: 11000.1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-269-0565
TELEFAX: 206-269-0563
TELEX:
INFORMATION FOR SEQ ID NO: 154:
SEQUENCE CHARACTERISTICS:
LENGTH: 748 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-997-080-154
Query Match 72.9%; Score 35; DB 2; Length 748;
Best Local Similarity 77.8%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPHETITAL 9
| | | | |
Db 405 GPHETHRAL 413

RESULT 7
US-08-997-362-154
; Sequence 154, Application US/08997362
; Patent No. 5985287
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Hiyama, Jun
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Scott, Linda
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF MYCOBACTERIAL INFECTIONS
; NUMBER OF SEQUENCES: 194
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
STREET: 2601 Elliott Avenue, Suite 4185
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,362
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/873,970
; FILING DATE: June 12, 1997
; APPLICATION NUMBER: U.S. Patent Application No. 5985287 08/705,347
; FILING DATE: August 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 154:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 748 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-997-362-154

Query Match 72.9%; Score 35; DB 2; Length 748;
Best Local Similarity 77.8%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPHETITAL 9
Db 405 GPHETHRAL 413

RESULT 8
US-09-095-855-154
; Sequence 154, Application US/09095855
; Patent No. 6160093
; GENERAL INFORMATION:
; APPLICANT: Tan, Paul
; APPLICANT: Visser, Elizabeth
; APPLICANT: Skinner, Margot
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Compounds and Methods for
; TITLE OF INVENTION: Treatment and Diagnosis of Mycobacterial Infections
; NUMBER OF SEQUENCES: 208
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Ann W. Speckman
; STREET: 2601 Elliott Avenue, Suite 4185
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/095,855
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/705,347
; FILING DATE: 29-AUG-1996
; APPLICATION NUMBER: 08/873,970
; FILING DATE: 12-JUN-1997
; APPLICATION NUMBER: 08/997,362
; FILING DATE: 23-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Sleath, Janet
; REGISTRATION NUMBER: 37,007
; REFERENCE/DOCKET NUMBER: 11000.1002c3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-269-0565
; TELEFAX: 206-269-0563
; TELEX:
; INFORMATION FOR SEQ ID NO: 154:
```

```
; SEQUENCE CHARACTERISTICS:
; LENGTH: 748 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-095-855-154

Query Match 72.9%; Score 35; DB 3; Length 748;
Best Local Similarity 77.8%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPHETITAL 9
Db 405 GPHETHRAL 413

RESULT 9
US-09-324-542-154
; Sequence 154, Application US/09324542
; Patent No. 6328978
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L.J.
; APPLICANT: Prestidge, Ross
; TITLE OF INVENTION: Methods and Compounds for the Treatment
; TITLE OF INVENTION: of Immunologically-Mediated Skin Disorders
; FILE REFERENCE: 11000.1007c1
; CURRENT APPLICATION NUMBER: US/09/324,542
; CURRENT FILING DATE: 1999-06-02
; EARLIER APPLICATION NUMBER: US 08/997,080
; EARLIER FILING DATE: 1997-12-23
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 154
; LENGTH: 748
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (119)...(119)
; US-09-324-542-154

Query Match 72.9%; Score 35; DB 3; Length 748;
Best Local Similarity 77.8%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPHETITAL 9
Db 405 GPHETHRAL 413

RESULT 10
US-09-205-426-154
; Sequence 154, Application US/09205426
; Patent No. 6406704
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Tan, Paul L. J.
; TITLE OF INVENTION: Compounds and Methods for Treatment and
; TITLE OF INVENTION: Diagnosis of Mycobacterial Infections
; FILE REFERENCE: 11000.1002c4
; CURRENT APPLICATION NUMBER: US/09/205,426
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: 09/095,855
; EARLIER FILING DATE: 1998-06-11
; EARLIER APPLICATION NUMBER: 08/997,362
; EARLIER FILING DATE: 1997-12-23
; EARLIER APPLICATION NUMBER: 08/873,970
; EARLIER FILING DATE: 1997-06-12
; EARLIER APPLICATION NUMBER: 08/705,347
; EARLIER FILING DATE: 1996-08-29
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 3.0
```

```

; SEQ ID NO 154
; LENGTH: 748
; TYPE: PRT
; ORGANISM: Mycobacterium vaccae
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (119)...(119)
US-09-205-426-154

Query Match 72.9%; Score 35; DB 4; Length 748;
Best Local Similarity 77.8%; Pred. No. 94;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPHETITAL 9
||| ||| ||
Db 405 GPHETITAL 413

RESULT 11
US-09-005-180A-3
; Sequence 3, Application US/09005180A
; Patent No. 6124446
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN VPS35/MEM3-RELATED PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/005.180A
; FILING DATE: Filed January 8, 1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PP-0457 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 754 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1354049
US-09-005-180A-3

Query Match 72.9%; Score 35; DB 3; Length 754;
Best Local Similarity 75.0%; Pred. No. 95;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PHETITAL 9
||| ||| ||
Db 523 PHETITAL 530

RESULT 12
US-09-513-999C-6366
; Sequence 6366, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513.999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 6366
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 13
; OTHER INFORMATION: Xaa=Ala or Glu
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 22
; OTHER INFORMATION: Xaa=Ala or Pro or Ser or Thr
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 88
; OTHER INFORMATION: Xaa=Cys or Ser
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 98
; OTHER INFORMATION: Xaa=Gly or Val
US-09-513-999C-6366

Query Match 70.8%; Score 34; DB 4; Length 102;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPHETITA 8
||| ||| ||
Db 4 GPHETATA 11

RESULT 13
US-09-615-192A-311
; Sequence 311, Application US/09615192A
; Patent No. 6410718
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; MODIFICATION OF PLANT LIGNIN CONTENT
; FILE REFERENCE: 11000.1003C4U
; CURRENT APPLICATION NUMBER: US/09/615.192A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 08/975,316
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 08/713,000
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: US 09/169,789
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 311
; LENGTH: 154
; TYPE: PRT
```

; ORGANISM: Pinus radiata
US-09-615-192A-311

Query Match 70.8%; Score 34; DB 4; Length 154;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PHETITAL 9
||:||||
Db 61 PHQAITAL 68

RESULT 14

US-09-134-000C-5791
; Sequence 5791, Application US/09134000C
; Patent No. 6617156

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 032796-032

; CURRENT APPLICATION NUMBER: US/09/134,000C

; CURRENT FILING DATE: 1998-08-13

; PRIOR FILING DATE: 1997-08-15

; NUMBER OF SEQ ID NOS: 6812

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 5791

; LENGTH: 300

; TYPE: PRT

; ORGANISM: Enterococcus faecalis

US-09-134-000C-5791

Query Match

Best Local Similarity 70.8%; Score 34; DB 4; Length 300;
Best Local Similarity 62.5%; Pred. No. 53;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 PHETITAL 9
||:||||
Db 28 PHQTLTSL 35

RESULT 15

US-09-252-991A-17077

; Sequence 17077, Application US/09252991A
; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 17077

; LENGTH: 699

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-17077

Query Match

Best Local Similarity 70.8%; Score 34; DB 4; Length 699;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPHETITAL 9
|||:||||
Db 347 GPHQPIVAL 355

RESULT 16

US-09-543-681A-5706

; Sequence 5706, Application US/09543681A

; Patent No. 6605709

; GENERAL INFORMATION:

; APPLICANT: GARY BRETON

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS

; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.1002-001

; CURRENT APPLICATION NUMBER: US/09/543,681A

; CURRENT FILING DATE: 2000-04-05

; PRIOR APPLICATION NUMBER: US 60/128,706

; PRIOR FILING DATE: 1999-04-09

; NUMBER OF SEQ ID NOS: 8344

; SEQ ID NO 5706

; LENGTH: 717

; TYPE: PRT

; ORGANISM: Proteus mirabilis

US-09-543-681A-5706

Query Match

Best Local Similarity 70.8%; Score 34; DB 4; Length 717;
Best Local Similarity 77.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPHETITAL 9
|||:||||
Db 497 GVHETINAL 505

RESULT 17

US-09-107-532A-4275

; Sequence 4275, Application US/09107532A

; Patent No. 6583275

; GENERAL INFORMATION:

; APPLICANT: Lynn A Doucette-Stamm and David Bush

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

; NUMBER OF SEQUENCES: 7310

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: GENOME THERAPEUTICS CORPORATION

; STREET: 100 Beaver Street

; CITY: Waltham

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02354

; COMPUTER READABLE FORM:

; MEDIUM TYPE: CD-ROM ISO9660

; COMPUTER: PC

; OPERATING SYSTEM: <Unknown>

; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/107,532A

; FILING DATE: 30-Jun-1998

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/085,598

; FILING DATE: 14 May 1998

; APPLICATION NUMBER: 60/051571

; FILING DATE: July 2, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Ariniello, Pamela Deneke

; REGISTRATION NUMBER: 40,489

; REFERENCE/DOCKET NUMBER: GTC-012

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (781)893-5007

; TELEFAX: (781)893-8277

; INFORMATION FOR SEQ ID NO: 4275:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 762 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: YES

; ORIGINAL SOURCE:

```

; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...762
; SEQUENCE DESCRIPTION: SEQ ID NO: 4275:
US-09-107-532A-4275
    Query Match          70.8%; Score 34; DB 4; Length 762;
    Best Local Similarity 66.7%; Pred. No. 1.5e+02;
    Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GPHETITAL 9
Db      383 GPHELINSL 391

RESULT 18
US-08-936-135-4
; Sequence 4, Application US/08936135
; Patent No. 6054293
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: He, Zhigang
; APPLICANT: Chen, Hang
; TITLE OF INVENTION: Semaphorin Receptors
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/936,135
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC97-288-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2584 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-936-135-4
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/936,135
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC97-288-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2584 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-936-135-4
    Query Match          70.8%; Score 34; DB 3; Length 2584;
    Best Local Similarity 66.7%; Pred. No. 6.2e+02;
    Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GPHETITAL 9
Db      1165 GPHGLVAL 1173

RESULT 19
US-08-936-135-2
; Sequence 2, Application US/08936135
; Patent No. 6054293
; GENERAL INFORMATION:
; APPLICANT: Tessier-Lavigne, Marc
; APPLICANT: He, Zhigang
; APPLICANT: Chen, Hang
; TITLE OF INVENTION: Semaphorin Receptors
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 75 DENISE DRIVE
; CITY: HILLSBOROUGH
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94010
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/936,135
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: OSMAN, RICHARD A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: UC97-288-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 343-4341
; TELEFAX: (650) 343-4342
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2584 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-936-135-2
    Query Match          70.8%; Score 34; DB 3; Length 2588;
    Best Local Similarity 66.7%; Pred. No. 6.2e+02;
    Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      1 GPHETITAL 9
Db      1167 GPHGLVAL 1175

RESULT 20
US-09-107-532A-7025
; Sequence 7025, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
```

```
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 7025:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 81 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...81
; SEQUENCE DESCRIPTION: SEQ ID NO: 7025:
US-09-107-532A-7025

Query Match 68.8%; Score 33; DB 4; Length 81;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PHETITAL 9
Db 37 PHMTITAI 44

RESULT 21
US-09-252-991A-22552
; Sequence 22552, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22552
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22552

Query Match 68.8%; Score 33; DB 4; Length 364;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GPHETITA 8
Db 31 GPHRTSTA 38

RESULT 22
US-09-248-796A-19514
; Sequence 19514, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
```

```
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19514
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (87)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown
US-09-248-796A-19514

Query Match 68.8%; Score 33; DB 4; Length 401;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PHETITAL 9
Db 114 PHSTISAL 121

RESULT 23
US-07-832-855-2
; Sequence 2, Application US/07832855
; Patent No. 5478727
; GENERAL INFORMATION:
; APPLICANT: Roizman, Bernard
; APPLICANT: Liu, Fenyong
; TITLE OF INVENTION: Methods and Compositions of a
; TITLE OF INVENTION: Preparation and Use of A Herpes Protease
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: 321 No. 5478727th Clark Street, Suite 800
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/832,855
; FILING DATE: 19920207
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coolley, Ronald B.
; REGISTRATION NUMBER: 27,187
; REFERENCE/DOCKET NUMBER: ARCD045
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 744-0090
; TELEFAX: (312) 245-4961
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 635 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-832-855-2

Query Match 68.8%; Score 33; DB 1; Length 635;
Best Local Similarity 77.8%; Pred. No. 2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPHETITAL 9
Db 473 GTNETITAL 481
```

RESULT 24
US-08-176-320-2
; Sequence 2, Application US/08176320
; Patent No. 6410704
; GENERAL INFORMATION:
; APPLICANT: Roizman, Bernard
; APPLICANT: Liu, Fenyong
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITLE OF INVENTION: PREPARATION AND USE OF A HERPES PROTEASE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Alice O. Martin
; STREET: 321 No. 6410704th Clark Street, Suite 800
; CITY: Chicago
; STATE: ILL
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/176.320
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/705.814
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooley, Ronald B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312)744-0090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 635 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-176-320-2

Query Match 68.8%; Score 33; DB 4; Length 635;
Best Local Similarity 77.8%; Pred. No. 2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GPHETITAL 9
|:|||||
Db 473 GNETITAL 481

RESULT 25
US-09-489-039A-8750
; Sequence 8750, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8750
; LENGTH: 726
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8750

Query Match 68.8%; Score 33; DB 4; Length 726;

Best Local Similarity 77.8%; Pred. No. 2.3e+02;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GPHETITAL 9
|:|||||
Db 507 GIHETINAL 515

RESULT 26
US-09-762-724-10
; Sequence 10, Application US/09762724
; Patent No. 6664053
; GENERAL INFORMATION:
; APPLICANT: Kovacs, et al.
; TITLE OF INVENTION: Identification of a region of the major surface
; TITLE OF INVENTION: glycoprotein (MSG) gene of human Pneumocystis carinii
; FILE REFERENCE: 4239-58054
; CURRENT APPLICATION NUMBER: US/09/762,724
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PCT/US99/18750
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: US 60/096,805
; PRIOR FILING DATE: 1998-08-17
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1009
; TYPE: PRT
; ORGANISM: Pneumocystis carinii sp. f. hominis
US-09-762-724-10

Query Match 68.8%; Score 33; DB 4; Length 1009;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PHETIT 7
|:|||||
Db 921 PHETVT 926

RESULT 27
US-09-762-724-12
; Sequence 12, Application US/09762724
; Patent No. 6664053
; GENERAL INFORMATION:
; APPLICANT: Kovacs, et al.
; TITLE OF INVENTION: Identification of a region of the major surface
; TITLE OF INVENTION: glycoprotein (MSG) gene of human Pneumocystis carinii
; FILE REFERENCE: 4239-58054
; CURRENT APPLICATION NUMBER: US/09/762,724
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PCT/US99/18750
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: US 60/096,805
; PRIOR FILING DATE: 1998-08-17
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1017
; TYPE: PRT
; ORGANISM: Pneumocystis carinii sp. f. hominis
US-09-762-724-12

Query Match 68.8%; Score 33; DB 4; Length 1017;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PHETIT 7
|:|||||
Db 912 PHETVT 917

RESULT 28

```
US-09-762-724-14
; Sequence 14, Application US/09762724
; Patent No. 6664053
; GENERAL INFORMATION:
; APPLICANT: Kovacs, et al.
; TITLE OF INVENTION: Identification of a region of the major surface
; FILE REFERENCE: 4239-58054
; CURRENT APPLICATION NUMBER: US/09/762,724
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PCT/US99/18750
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: US 60/096,805
; PRIOR FILING DATE: 1998-08-17
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 1023
; TYPE: PRT
; ORGANISM: Pneumocystis carinii sp. f. hominis
US-09-762-724-14
Query Match 68.8%; Score 33; DB 4; Length 1023;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PHETIT 7
Db 916 PHETVT 921

RESULT 29
US-09-762-724-8
; Sequence 8, Application US/09762724
; Patent No. 6664053
; GENERAL INFORMATION:
; APPLICANT: Kovacs, et al.
; TITLE OF INVENTION: Identification of a region of the major surface
; FILE REFERENCE: 4239-58054
; CURRENT APPLICATION NUMBER: US/09/762,724
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: PCT/US99/18750
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: US 60/096,805
; PRIOR FILING DATE: 1998-08-17
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1027
; TYPE: PRT
; ORGANISM: Pneumocystis carinii sp. f. hominis
US-09-762-724-8
Query Match 68.8%; Score 33; DB 4; Length 1027;
Best Local Similarity 83.3%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PHETIT 7
Db 922 PHETVT 927

RESULT 30
US-09-513-999C-5317
; Sequence 5317, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
```

```
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5317
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 46
; OTHER INFORMATION: Xaa=Glu or Gly
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 48
; OTHER INFORMATION: Xaa=Lys or Asn
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 55
; OTHER INFORMATION: Xaa=Asp or Glu
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 88
; OTHER INFORMATION: Xaa=Ile or Met
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 91
; OTHER INFORMATION: Xaa=Ala or Pro
US-09-513-999C-5317
Query Match 66.7%; Score 32; DB 4; Length 108;
Best Local Similarity 85.7%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GPHEIT 7
Db 96 GPHEIT 102

RESULT 31
US-09-007-484-4
; Sequence 4, Application US/09007484
; Patent No. 6072032
; GENERAL INFORMATION:
; APPLICANT: Black, Michael T.
; TITLE OF INVENTION: No. 6072032el Ftsy
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
; CITY: Philadelphia
; STATE: PA
; COUNTRY: US
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/007,484
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Falk, Stephen T
; REGISTRATION NUMBER: 36,795
; REFERENCE/DOCKET NUMBER: GM10081
```

TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-994-2488
; TELEFAX: 215-994-2222
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-007-484-4

Query Match 66.7%; Score 32; DB 3; Length 277;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PHETITAL 9
Db 192 PHETFLAL 199

RESULT 32
US-09-309-682-4
; Sequence 4, Application US/09309682
; Patent No. 6214348
; GENERAL INFORMATION:
; APPLICANT: Black, Michael T.
; TITLE OF INVENTION: No. 6214348el Ftsy
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
; CITY: Philadelphia
; STATE: PA
; COUNTRY: US
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/309,682
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/007,484
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Falk, Stephen T.
; REGISTRATION NUMBER: 36,795
; REFERENCE/DOCKET NUMBER: GM10081
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-994-2488
; TELEFAX: 215-994-2222
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-309-682-4

Query Match 66.7%; Score 32; DB 3; Length 277;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PHETITAL 9
Db 192 PHETFLAL 199

RESULT 33
US-09-335-409-22
; Sequence 22, Application US/09335409
; Patent No. 6121029
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/335,409
; CURRENT FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-335-409-22

Query Match 66.7%; Score 32; DB 3; Length 305;
Best Local Similarity 55.6%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GPHEITITAL 9
Db 250 GPHEVLVVL 258

RESULT 34
US-09-568-102-22
; Sequence 22, Application US/09568102
; Patent No. 6346404
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568,102
; CURRENT FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/335,409
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-568-102-22

Query Match 66.7%; Score 32; DB 3; Length 305;
Best Local Similarity 55.6%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GPHEITITAL 9
Db 250 GPHEVLVVL 258

RESULT 35
US-09-567-969-22
; Sequence 22, Application US/09567969
; Patent No. 6355457
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James

```
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/567,969
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/335,409
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-567-969-22

Query Match      66.7%; Score 32; DB 3; Length 305;
Best Local Similarity 55.6%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 GPHETITAL 9
Db      250 GPHEVLVWL 258

RESULT 36
US-09-568-480-22
; Sequence 22, Application US/09568480
; Patent No. 6355458
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568,480
; PRIOR FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/335,409
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-568-480-22

Query Match      66.7%; Score 32; DB 3; Length 305;
Best Local Similarity 55.6%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 GPHETITAL 9
Db      250 GPHEVLVWL 258

RESULT 37
US-09-568-486-22
; Sequence 22, Application US/09568486
; Patent No. 6355459
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
```

```
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568,486
; CURRENT FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/335,409
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-568-486-22

Query Match      66.7%; Score 32; DB 3; Length 305;
Best Local Similarity 55.6%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 GPHETITAL 9
Db      250 GPHEVLVWL 258

RESULT 38
US-09-568-472-22
; Sequence 22, Application US/09568472
; Patent No. 6358719
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/568,472
; CURRENT FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/335,409
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-568-472-22

Query Match      66.7%; Score 32; DB 3; Length 305;
Best Local Similarity 55.6%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 GPHETITAL 9
Db      250 GPHEVLVWL 258

RESULT 39
US-09-567-899-22
; Sequence 22, Application US/09567899
; Patent No. 6383787
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/09/567,899
; CURRENT FILING DATE: 2000-05-10
; PRIOR APPLICATION NUMBER: 09/335,409
; PRIOR FILING DATE: 1999-06-17
```

; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 305
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-567-899-22

Query Match 66.7%; Score 32; DB 3; Length 305;
Best Local Similarity 55.6%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GPHETITAL 9
| | | | |
Db 250 GPHEVLVL 258

RESULT 40
US-09-328-352-4994
; Sequence 4994, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4994
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4994

Query Match 66.7%; Score 32; DB 4; Length 307;
Best Local Similarity 85.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GPHETIT 7
| | | | |
Db 124 GPHLTIT 130

RESULT 41
US-09-902-540-11852
; Sequence 11852, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11852
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11852

Query Match 66.7%; Score 32; DB 4; Length 315;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 PHETITAL 9
| | | | |
Db 35 PHETVEAV 42

us-10-623-429-9_copy_475_483.rai

RESULT 42
US-09-489-039A-12482
; Sequence 12482, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12482
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12482

Query Match 66.7%; Score 32; DB 4; Length 383;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPHETITAL 9
| | | | |
Db 276 GVHETITEL 284

RESULT 43
US-08-986-963-2
; Sequence 2, Application US/08986963
; Patent No. 5958730
; GENERAL INFORMATION:
; APPLICANT: Rosteck Jr., Paul R.
; TITLE OF INVENTION: Streptococcus Pneumoniae Gene Sequence
; TITLE OF INVENTION: PtsY
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: US
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/986,963
; APPLICATION NUMBER: US/08/986,963
; FILING DATE: December 8, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Webster, Thomas D.
; REGISTRATION NUMBER: 39,872
; REFERENCE/DOCKET NUMBER: X-11763
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317/276-3334
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 425 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-986-963-2

Query Match 66.7%; Score 32; DB 2; Length 425;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY      2 PHETITAL 9
      |||||
Db      340 PHETFLAL 347

RESULT 44
US-09-583-110-4561
; Sequence 4561, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 60/051,553
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 4561
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4561

Query Match      66.7%; Score 32; DB 4; Length 429;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 PHETITAL 9
      |||||
Db      344 PHETFLAL 351

RESULT 45
US-09-007-484-2
; Sequence 2, Application US/09007484
; Patent No. 6072032
; GENERAL INFORMATION:
; APPLICANT: Black, Michael T.
; TITLE OF INVENTION: No. 6072032e1 FtsY
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
; CITY: Philadelphia
; STATE: PA
; COUNTRY: US
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/007,484
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/007,484
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Falk, Stephen T.
; REGISTRATION NUMBER: 36,795
; REFERENCE/DOCKET NUMBER: GM10081
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-994-2488
; TELEFAX: 215-994-2222
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 430 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-309-682-2

Query Match      66.7%; Score 32; DB 3; Length 430;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 PHETITAL 9
      |||||
Db      345 PHETFLAL 352

RESULT 46
US-09-309-682-2
; Sequence 2, Application US/09309682
; Patent No. 6214348
; GENERAL INFORMATION:
; APPLICANT: Black, Michael T.
; TITLE OF INVENTION: No. 6214348e1 FtsY
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
; CITY: Philadelphia
; STATE: PA
; COUNTRY: US
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/309,682
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/007,484
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Falk, Stephen T.
; REGISTRATION NUMBER: 36,795
; REFERENCE/DOCKET NUMBER: GM10081
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-994-2488
; TELEFAX: 215-994-2222
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 430 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-309-682-2

Query Match      66.7%; Score 32; DB 3; Length 430;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 PHETITAL 9
      |||||
Db      345 PHETFLAL 352

RESULT 47
US-09-107-433-2686
; Sequence 2686, Application US/09107433
```

Patent No. 6800744
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTICS
AND THERAPEUTICS
NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
SOFTWARE: <Unknown>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneka
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 2686:
SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae
FEATURE:
NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...430
SEQUENCE DESCRIPTION: SEQ ID NO: 2686:
US-09-107-433-2686
Query Match 66.7%; Score 32; DB 4; Length 430;
Best Local Similarity 75.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 2 PHETITAL 9
DB 345 PHETITAL 352
RESULT 48
US-09-540-236-2280
Sequence 2280, Application US/09540236
Patent No. 6673910
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
FILE REFERENCE: 2709, 2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2280
LENGTH: 431
TYPE: PRT

ORGANISM: M. catarrhalis
US-09-540-236-2280
Query Match 66.7%; Score 32; DB 4; Length 431;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 GPHEITITAL 9
DB 179 GEHQAITAL 187
RESULT 49
US-09-413-814-72
Sequence 72, Application US/09413814
Patent No. 6225064
GENERAL INFORMATION:
APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
APPLICANT: Bristol-Myers Squibb, Co.
APPLICANT: Beyer, Stefan
APPLICANT: Bloecker, Helmut
APPLICANT: Brandt, Petra
APPLICANT: Cino, Paul M
APPLICANT: Dougherty, Brian A
APPLICANT: Goldberg, Steven L
APPLICANT: Hofle, Gerhard
APPLICANT: Mueller, Joachim
APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polypeptide or
TITLE OF INVENTION: heteropolypeptide compounds
FILE REFERENCE: PCT/US 95/23535
CURRENT APPLICATION NUMBER: US/09/413,814
CURRENT FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: DE 198 46 493.2
EARLIER FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 72
LENGTH: 492
TYPE: PRT
ORGANISM: Sorangium cellulosum
US-09-413-814-72
Query Match 66.7%; Score 32; DB 3; Length 492;
Best Local Similarity 55.6%; Pred. No. 2.4e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 1 GPHEITITAL 9
DB 437 GPHEVLVVL 445
RESULT 50
US-09-328-352-7300
Sequence 7300, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER BAUMANNII
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7300
LENGTH: 536
TYPE: PRT
ORGANISM: Acinetobacter baumannii
US-09-328-352-7300
Query Match 66.7%; Score 32; DB 4; Length 536;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GPHETITAL 9
| | | | |
Db 285 GERQAITAL 293

Search completed: July 27, 2005, 12:42:50
Job time : 53 secs